VONDERHEIDE, Robert, H. [US/US]; Apartment 801,
1284 Beacon Street, Brookline, MA 02115 (US).

(74) Agent: CLARK, Paul, T.; Clark & Elbing LLP, 176 Federal
Street, Boston, MA 02110–2214 (US).

(54) Title: CANCER IMMUNOTHERAPHY AND DIAGNOSIS USING UNIVERSAL TUMOR ASSOCIATED ANTIGENS, INCLUD-
ING hTERT

(57) Abstract

The invention provides methods for conducting cancer immonotherapy and diagnosis using universal tumor associated antigens, such as the telomerase catalytic subunit (hTERT), and methods for identifying and characterizing universal tumor associated antigens.

CANCER IMMUNOTHERAPHY AND DIAGNOSIS USING UNIVERSAL TUMOR ASSOCIATED ANTIGENS, INCLUD-
ING hTERT

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Background of the Invention

This invention relates to methods of identifying universal tumor associated antigens, and use of such antigens in the prevention, treatment, and

10   diagnosis of cancer.

The paucity of clinically significant anti-tumor immune responses in cancer patients has long suggested that antigen-specific immunotherapy would not play a significant role in cancer treatment. However, pioneering studies in the early 1990s, using tumor-specific cytotoxic T lymphocytes (CTLs) from

15   cancer patients, showed the existence of human tumor associated antigens (TAAs), suggesting that such antigens could be used to stimulate therapeutic anti-tumor immune responses in patients. Although these studies primarily focused on melanoma, TAAs have been subsequently characterized in several other malignancies, raising the hypothesis that most, if not all, tumors express

20   antigens that can be used to induce CTL-mediated tumor destruction. Consequently, exciting clinical efforts are now underway to target these TAAs in strategies such as vaccination and adoptive T cell therapy to generate effective anti-tumor CTL responses in patients.

Unfortunately, most TAAs described thus far are expressed in only

25   one or a few tumor types, and not all patients with a given tumor type express the associated TAA. As a result, progress in the field of cancer immunotherapy has been relatively slow, because it has not been possible to develop widely useful TAA-specific immunotherapeutic strategies. Not only has it been

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necessary to tailor such therapies to individual types of malignancies, in some
cases (such as the immunoglobulin idiotypic antigen in B cell malignancies), it
has been necessary to tailor these therapies to individual patients.

More than 85% of human cancers display telomerase activity (Kim *et
al.*, Science 266:2011-2015, 1994). Telomerase is a ribonucleoprotein complex
that maintains the telomeric ends of linear chromosomes, thus protecting them
from degradation and end-to-end fusion. The human telomerase complex
contains a reverse transcriptase, known as hTERT, and an RNA component that
is used as a template for telomere synthesis by hTERT. The hTERT subunit is
the rate-limiting component of the complex, and its expression correlates best
with telomerase activity. Most human cells do not express hTERT or display
telomerase activity, and therefore lose telomeric DNA with each cell division.
In contrast, more than 85% of human tumors express hTERT, exhibit strong
telomerase activity, and maintain the length of their telomeres, suggesting that
the activation of telomerase plays an important role in the development of
human cancers.

Summary of the Invention

The invention provides a method of treating a patient that has or is at
risk of having a cell that expresses hTERT. This method involves
administering to the patient a cytotoxic T lymphocyte (CTL)(autologous or
allogeneic) that kills the cell in an hTERT-specific, major histocompatibility
complex-restricted fashion. The CTL can be generated, for example, by
activation with an antigen presenting cell that has been pulsed with hTERT, or
a peptide of hTERT that binds to a major histocompatibility complex molecule.

The invention also includes a second method of treating a patient that
has or is at risk of having a cell that expresses hTERT. This method involves

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administering to the patient an antigen presenting cell (APC) that activates in

the patient a cytotoxic T lymphocyte that kills the cell in an hTERT-specific,

major histocompatibility complex-restricted fashion. The APC can be pulsed

with hTERT or a peptide of hTERT that binds to a major histocompatibility

5   complex molecule.

Another method included in the invention is a third method of

treating a patient that has or is at risk of having a cell that expresses hTERT.

This method involves administering to the patient hTERT or a peptide of

hTERT that binds to a major histocompatibility complex molecule, which is

10   processed by an antigen presenting cell in the patient, which, in turn, activates a

cytotoxic T lymphocyte in the patient to kill the cell that expresses hTERT in

an hTERT-specific, major histocompatibility complex-restricted fashion. The

hTERT or peptide of hTERT used in this method can be administered to the

patient in association with an adjuvant.

15   The invention also includes a fourth method of treating a patient that

has is at risk of having a cell that expresses hTERT. This method involves

administering to the patient a nucleic acid molecule encoding hTERT or a

peptide of hTERT that binds to a major histocompatibility complex molecule.

The nucleic acid molecule is expressed in the patient so that it can be processed

20   by an antigen presenting cell in the patient, which activates a cytotoxic T

lymphocyte in the patient to kill the cell that expresses hTERT in an hTERT-

specific, major histocompatibility complex-restricted fashion. The nucleic acid

molecule encoding hTERT or a peptide of hTERT can be present in an

expression vector.

25   In any of the methods described above, the patient can have a tumor

containing cells that express hTERT. APCs used in these methods can be, for

example, a dendritic cell or a CD40-activated B cell. The peptide of hTERT in

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these methods can bind to a class I or a class II major histocompatibility

complex (MHC) molecule. In the case of a class I MHC molecule, the

molecule can be an HLA-A2 molecule or an HLA-A3 molecule (also see

below). In the case of an HLA-A2 molecule, the peptide of hTERT can include

5   the amino acid sequence of SEQ ID NO:1. In the case of an HLA-A3

molecule, the peptide of hTERT can include the amino acid sequence of SEQ

ID NO:2. Examples of other hTERT sequences that can be used in these

methods are listed below.

          The invention also includes a method of assessing the level of

10   immunity of a patient to hTERT or a peptide of hTERT that binds to a major

histocompatibility complex molecule. In this method, the level of cytotoxic T

lymphocytes specific for hTERT or a peptide of hTERT is measured in a

sample from the patient. The sample can be obtained from the patient before,

during, or after a cancer treatment is administered to the patient. A sample can

15   also be obtained, for example, before and after treatment.

          The invention also includes an hTERT peptide that binds to a major

histocompatibility complex molecule, for example, a peptide that consists

essentially of the amino acid sequence set forth in SEQ ID NO:1 or SEQ ID

NO:2 (also see below).

20   Also included in the invention is an *ex vivo* generated cytotoxic T

lymphocyte that specifically kills a cell expressing hTERT in a specific, major

histocompatibility complex-restricted fashion, and an *ex vivo* generated antigen

presenting cell (e.g., a dendritic cell or a CD40-activated B cell) that presents a

peptide of a hTERT in the context of a major histocompatibility complex

25   molecule.

          The invention also includes a method for identifying a universal

tumor associated antigen. This method involves: (a) analyzing one or more

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databases to identify a gene that is: (i) expressed in more than one human tumor type, and (ii) expressed in at least one human tumor type at a level that is at least 3-fold (e.g., 5-fold or 10-fold) higher than the level at which it is expressed in a normal human cell; (b) using a computer-run algorithm to

5   identify an amino acid sequence in the protein encoded by the gene that is predicted bind to a major histocompatibility complex molecule (e.g., a class I or class II major histocompatibility molecule); (c) synthesizing an immunogen that comprises the amino acid sequence identified in step (b), or a sequence that is predicted by a computer-run algorithm to bind to a major histocompatibility

10   complex molecule with higher affinity than the sequence; and (d) testing the ability of the immunogen to stimulate a major histocompatibility complex-restricted cytotoxic T lymphocyte response that is specific for the protein.

The peptide, preferably, is predicted to bind to MHC with a probability of at least, e.g., 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100%.

15   It also, preferably, binds to MHC with at least intermediate affinity (e.g., with an IC50 of about 51-500 nM), for example, with high affinity (e.g., with an IC50 of up to 50 nM).

This method can also include, after step (d), testing the ability of a major histocompatibility complex-restricted cytotoxic T lymphocyte that is

20   specific for the universal tumor associated antigen and is generated in step (d) to kill a malignant cell expressing the universal tumor associated antigen and not a non-malignant cell.

Also, the method can include, after step (c) and prior to step (d), using a time-resolved, fluorometry-based assay to measure MHC binding and

25   MHC/peptide complex stability of a peptide comprising the amino acid sequence identified in step (b).

The testing of the immunogen can be carried out by contacting a

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cytotoxic T lymphocyte with an antigen presenting cell (*e.g.*, a dendritic cell or a CD40-activated B cell) that has been pulsed with the immunogen.

The methods of the invention described above with respect to hTERT can also be carried out with any universal tumor associated antigens or

5   MHC-binding peptides thereof that are identified using the above-described method. Also, the invention includes a universal tumor-associated antigen or a peptide thereof that binds to a major histocompatibility complex molecule; an *ex vivo* generated cytotoxic T lymphocyte that specifically kills a cell expressing a universal tumor-associated antigen in a specific, major

10 histocompatibility complex-restricted fashion; and an *ex vivo* generated antigen presenting cell that presents a peptide of a universal tumor-associated antigen in the context of a major histocompatibility complex molecule.

As is understood in the art, a "polypeptide" is a chain of amino acids linked to one another by peptide bonds. A "protein" can be made up of one or

15 more polypeptides, while a "peptide" is generally understood to be (or include) a fragment of a polypeptide, and to consist of a chain of peptide bond-linked amino acids that is shorter in length than a full length polypeptide from which it may be derived.

A "tumor associated antigen" is an immunogenic molecule, such as a

20 protein, that is, generally, expressed at a higher level in tumor cells than in non-tumor cells, in which, preferably, it may not be expressed at all, or only at low levels. A tumor associated antigen, or TAA, is said to be "universal" if it is expressed in tumors of different origins. For example, as is discussed above, the catalytic subunit of telomerase, hTERT, is expressed in more than 85% of

25 human cancers, and thus is a universal tumor antigen. Other antigens qualifying as universal TAAs could be, for example, expressed in at least three, for example, four, five, six, seven, eight, or more different types of tumors.

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A "tumor associated antigen polypeptide," or a "TAA polypeptide" is a full length, non-fragmented polypeptide of a tumor associated antigen, while a "tumor associated antigen peptide," or a "TAA peptide," is (or includes) a fragment of such a TAA polypeptide. TAA peptides can be of any

5   length, up to just under the full length of a TAA polypeptide. However, preferably, for use in the invention, TAA peptides are of a relatively short length, such as, for example, eight, nine, ten, eleven, or twelve amino acids. Also, a TAA peptide may include sequences that are not present in a corresponding TAA polypeptide, provided that the TAA peptide also includes a

10   stretch of at least, for example, eight, nine, ten, eleven, or twelve consecutive amino acids that have a sequence that is identical to a sequence of eight, nine, ten, eleven, or twelve consecutive amino acids in a TAA polypeptide.

Peptides including amino acid substitutions can also be considered as TAA peptides. For example, a TAA peptide can include a region of at least

15   nine amino acids, of which any six or more are identical to the amino acids within a nine amino acid stretch in a given TAA. Preferably, at least seven, more preferably, at least eight, and, most preferably, all nine of the amino acids in a TAA peptide nine amino acid region are identical to a nine amino acid region in the TAA.

20   A TAA polypeptide corresponding to hTERT includes 1132 amino acids that are substantially identical (see below) to the amino acid sequence of hTERT, or such a polypeptide can include the amino acid sequence of hTERT, as well as additional sequences.

As is discussed further below, it is preferable that TAA polypeptides

25   of the invention include regions that bind to major histocompatibility complex (MHC) antigens. Similarly, it is preferable that TAA peptides of the invention bind to MHC antigens.

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By "hTERT" is meant the catalytic subunit of human telomerase (see, *e.g.*, Genbank Accession No. AF018167). Preferred examples of hTERT peptides that are included in the invention are the peptides I540 (SEQ ID NO:1) and K973 (SEQ ID NO:2), as described herein. Additional hTERT peptides are
5   described below, and still more hTERT peptides can be identified using methods described below.

A TAA (*e.g.*, hTERT) peptide or polypeptide can be fused to amino acid sequences that do not naturally occur in the TAA. Moreover, a TAA peptide or polypeptide can be attached to the surface of a cell or to a molecule
10 or a macromolecule (*e.g.*, a histocompatibility antigen), or a TAA peptide or polypeptide can be conjugated to immunogens or adjuvants that are known to those of skill in this art, for example, keyhole limpet hemocyanin (KLH), for the purpose of eliciting a TAA-specific immune response. Preferred examples of hTERT peptides are the peptides I540 (SEQ ID NO:1) and K973 (SEQ ID
15 NO:2), as described herein.

By "TAA nucleic acid molecule" is meant a DNA or RNA (*e.g.*, mRNA) molecule that encodes a TAA peptide or TAA polypeptide, as are defined above.

By "TAA-expressing tumor cell" is meant a tumor cell that expresses
20 a given TAA (*e.g.*, hTERT). A TAA-expressing tumor cell can express a level of TAA that is equal to, or, preferably, greater than the level of TAA expressed by the normal cell type from which the TAA-expressing tumor cell has originated, or other non-tumor cells. Preferably, the tumor cell expresses at least 10% more TAA, more preferably, at least 25% more, still more preferably
25 at least 50% more, and most preferably at least 150% more TAA than the normal cell type from which the TAA-expressing tumor cell has originated, or another non-tumor cell. TAA expression levels in a TAA-expressing tumor

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cell can be increased by, for example, increased transcription of the TAA gene, increased TAA mRNA stability or translation, increased TAA polypeptide stability, or increased TAA enzymatic activity. Increasing such TAA expression levels may be useful in the invention to increase the likelihood that

5   a tumor cell will be recognized as a target of the immunotherapeutic methods described herein.

By "histocompatibility antigen" is meant a molecule, such as a major histocompatibility complex (MHC) class I, MHC class II, or minor histocompatibility antigen, that mediates interactions of cells of the immune

10   system with each other and with other cell types. Examples of histocompatibility antigens include MHC class I antigens, such as HLA-A (*e.g.*, A1, A2, A3, A11, A24, A31, A33, and A38), -B, and -C, MHC class II antigens, such as HLA-DR,-DQ, -DX, -DO, -DZ, and -DP, and minor histocompatibility antigens, such as HA-1.

15   By "generating CTLs" is meant an *in vivo*, *in vitro*, or *ex vivo* process by which TAA (*e.g.*, hTERT)-specific CTLs are activated (*e.g.*, stimulated to grow and divide) and/or selected.

A peptide of a TAA, such as hTERT, is said to "specifically bind" to an MHC antigen if the peptide adheres to a histocompatibility antigen under

20   physiological conditions. For example, such binding can be similar to that of a peptide antigen that is naturally processed and presented in the context of MHC in an antigen presenting cell.

A cytotoxic T lymphocyte (CTL) or antibody is said to "specifically recognize" a TAA polypeptide (*e.g.*, hTERT) or a TAA peptide if it binds to

25   the polypeptide or peptide, but does not substantially bind to other, unrelated polypeptides or peptides.

A CTL is said to "specifically kill" a cell if it specifically recognizes

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and lyses a cell that expresses a TAA (*e.g.*, hTERT) to which it has been

activated, but does not substantially recognize or lyse cells not expressing the

TAA. Such a CTL is designated as a "TAA-specific CTL" herein.

By "TAA-specific antibody" is meant an antibody that can

5   specifically recognize and bind to a TAA (*e.g.*, hTERT) peptide or polypeptide,

and does not substantially recognize and bind to other, unrelated molecules.

A TAA (*e.g.*, hTERT) is "presented" if a peptide of the TAA is

displayed on the extracellular surface of a cell (*e.g.*, an antigen presenting cell),

such that it can result in the *in vivo*, *ex vivo*, or *in vitro* generation of TAA-

10   specific CTLs or the lysis of a tumor cell by a TAA-specific CTL. Preferably,

the displayed TAA peptide is bound to a histocompatibility antigen.

By "physiological conditions" is meant the *in vivo* environment in

which TAA (*e.g.*, hTERT)-specific CTLs are generated (activated and/or

selected) and perform their biological functions (*e.g.*, recognition of the TAA

15   peptide and MHC-restricted lysis of TAA-expressing tumor cells), or an *in*

vitro or *ex vivo* environment that allows TAA-specific CTLs to be generated

and to perform their biological functions.

By "vaccination" is meant administration of an immunogenic

preparation including one or more TAA (*e.g.*, hTERT) peptides, TAA

20   polypeptides, TAA nucleic acid molecules, fragments of any of these

molecules, TAA-presenting cells (*e.g.*, dendritic cells or CD40-activated B

cells), or mixtures thereof. Vaccination is performed on a subject who has a

tumor, has a history of having a tumor or tumors, or is likely to develop a

tumor, or to a subject in which TAA-specific immune cells (such as CTLs) are

25   to be generated for transfer into a patient. Vaccination stimulates a TAA-

specific immune response within the subject. In subjects having tumors, the

vaccination can result in partial or complete inhibition of tumor growth, or

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partial or complete tumor regression, provided that the patient's tumor

expresses the TAA. In addition, vaccination can provide prophylaxis against

the development of new TAA-expressing tumors.

A "vaccine," as used herein, is an immunogenic composition that can

5   be administered in the vaccination method described above. Thus, a vaccine

includes, for example, one or more TAA (*e.g.*, hTERT) peptides, TAA

polypeptides, TAA nucleic acid molecules, fragments of any of these

molecules, TAA-presenting cells (*e.g.*, dendritic cells or CD40-activated B

cells), or mixtures thereof. Optionally, a vaccine composition can also include

10   an adjuvant, which is a molecule that stimulates an immune response to the co-

administered vaccine antigen. Examples of adjuvants that can be used in the

invention are provided below.

By "immune cell" is meant any cell that plays a role in cell-mediated

or humoral immunity, including CTLs and antigen-presenting cells, *e.g.*, B

15   cells, T helper cells, and dendritic cells.

By "sample" is meant a tumor or tissue biopsy, a lymph node biopsy,

bone marrow, cells, blood, serum, urine, stool, sputum, saliva, or other

specimen obtained from a patient. A sample can be analyzed to determine the

level of TAA (*e.g.*, hTERT)-specific CTLs, the level of TAA-specific

20   antibodies, or the level of any other immune response indicator (*e.g.*, cytokine

level) in the patient from whom it was taken, by methods that are known in the

art. For example, ELISA can be used to measure levels of TAA-specific

antibodies, and ELISPOT can be used to measure cytokine levels. Also, Cr^{51}

release (T cell cytotoxicity) assays and assays that test the binding of CTLs to

25   tetrameric TAA peptide/MHC complexes, as described herein, can be used to

measure levels of TAA-specific CTLs.

By "reference sample" is meant a sample in which the levels of TAA

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(e.g., hTERT)-specific CTLs or the level of TAA-specific antibodies have been measured, and to which the level of TAA-specific CTLs or the level of TAA-specific antibodies in a test subject's sample are compared. Reference levels can be higher, lower, or the same as patient sample levels. Comparison of a

5   test sample to a reference sample provides an assessment of the TAA-specific immune response in the test subject. In addition, comparison of a patient's sample levels to reference sample levels can allow a diagnosis of cancer and/or a prognosis of a cancer, in a patient having a tumor that comprises TAA-expressing cells.

10   By "cancer treatment" is meant any therapy (e.g., chemotherapy, radiation therapy, administration of TAA (e.g., hTERT)-specific CTLs, administration of an APC presenting a peptide of a TAA, or vaccination with a TAA, a nucleic acid molecule encoding a TAA, or a fragment thereof, to enhance an anti-tumor immune response) administered either alone or in

15 combination with other therapies, that alleviates disease in at least some patients to which the treatment is administered. For example, a cancer treatment can reduce or inhibit tumor growth, or can induce partial or complete tumor regression. Furthermore, a cancer treatment can be prophylactic, in that it inhibits or prevents the development of new tumors in patients that are in

20 remission from cancer, have metastatic cancer, or have a high risk of developing cancer.

By "inhibiting the development of a tumor" is meant administering a protective therapy (such as TAA (e.g., hTERT)-specific CTLs, TAA peptide presenting APCs, or a vaccine including, for example, one or more TAA

25 peptides, TAA polypeptides, or TAA nucleic acid molecules, or a combination thereof) to a subject adjudged to have a higher than average risk of developing a tumor. Subjects with a relatively high risk of developing a tumor include

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those having a family history of cancer, those having one or more genetic

mutations that are associated with a high risk for cancer (*e.g.*, a mutation that

inactivates a tumor suppressor gene), those having relatively high levels of

TAA-specific CTLs or TAA-specific antibodies, those who have cancer or are

5   in remission from cancer, and those who have been exposed to agents known or

suspected to cause cancer.

       By "pharmaceutically acceptable carrier" is meant a carrier that is

physiologically acceptable to a treated patient, while retaining the therapeutic

properties of the compound with which it is administered. One exemplary

10   pharmaceutically acceptable carrier is physiological saline. Other

physiologically acceptable carriers and their formulations are known to one

skilled in the art, and described, for example, in *Remington's Pharmaceutical*

Sciences (18th edition), ed. A. Gennaro, 1990, Mack Publishing Company,

Easton, PA.

15   By "substantially identical" is meant a polypeptide or nucleic acid

molecules exhibiting at least 50%, preferably at least 85%, more preferably at

least 90%, and most preferably at least 95% identity to a reference amino acid

or nucleic acid sequence. For polypeptides, the length of comparison

sequences is at least 16 amino acids, preferably at least 20 amino acids, more

20   preferably at least 25 amino acids, and most preferably 35 amino acids. For

nucleic acid molecules, the length of comparison sequences is at least 50

nucleotides, preferably at least 60 nucleotides, more preferably at least 75

nucleotides, and most preferably at least 110 nucleotides. Sequence identity is

typically measured using sequence analysis software with the default

25   parameters specified therein (*e.g.*, Sequence Analysis Software Package of the

Genetics Computer Group, University of Wisconsin Biotechnology Center,

1710 University Avenue, Madison, WI 53705). The TAA polypeptides,

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peptides, and nucleic acid molecules of the invention can be identical or
substantially identical to naturally occurring molecules, and thus may or may
not include non-wild type sequences.

By "substantially pure peptide" or "substantially pure polypeptide" is

5   meant a peptide, polypeptide, or a fragment thereof, that has been separated
from the components that naturally accompany it. Typically, the peptide or
polypeptide is substantially pure when it is at least 60%, by weight, free from
the proteins and naturally-occurring organic molecules with which it is
naturally associated. Preferably, the peptide or polypeptide is a TAA (*e.g.*,

10   hTERT) peptide or polypeptide that is at least 75%, more preferably at least
90%, and most preferably at least 99%, by weight, pure. A substantially pure
TAA peptide or polypeptide can be obtained, for example, by extraction from a
natural source (*e.g.*, a tumor cell), by expression of a recombinant nucleic acid
molecule encoding a TAA (*e.g.*, hTERT) peptide or polypeptide, or by

15   chemically synthesizing the peptide or polypeptide. Purity can be measured by
any appropriate method, *e.g.*, by column chromatography, polyacrylamide gel
electrophoresis, or HPLC analysis.

A protein is substantially free of naturally associated components
when it is separated from those contaminants that accompany it in its natural

20   state. Thus, a protein that is chemically synthesized or produced in a cellular
system different from the cell from which it naturally originates is substantially
free from its naturally associated components. Accordingly, substantially pure
peptides and polypeptides not only include those derived from eukaryotic
organisms but also those synthesized in *E. coli* or other prokaryotes.

25   By "substantially pure DNA" or "isolated DNA" is meant DNA that
is free of the genes that, in the naturally-occurring genome of the organism
from which the DNA is derived, flank the gene. The term thus includes, for

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example, a recombinant DNA that is incorporated into a vector; an autonomously replicating plasmid or virus; or the genomic DNA of a prokaryote or eukaryote; or DNA that exists as a separate molecule (*e.g.*, a cDNA, or a genomic or cDNA fragment produced by PCR or restriction

5   endonuclease digestion) independent of other sequences. It also includes a recombinant DNA that is part of a hybrid gene encoding additional polypeptide sequence.

By "transformation" is meant any method for introducing foreign molecules into a cell. Lipofection, DEAE-dextran-mediated transfection,

10   microinjection, protoplast fusion, calcium phosphate precipitation, transduction (*e.g.*, bacteriophage, adenoviral retroviral, or other viral delivery), electroporation, and biolistic transformation are just a few of the methods known to those skilled in the art which can be used in the invention.

By "transformed cell," "transfected cell," or "transduced cell," is

15   meant a cell (or a descendent of a cell) into which a nucleic acid molecule (*e.g.*, a DNA or RNA molecule) encoding a polypeptide of the invention has been introduced, by means of recombinant DNA techniques.

By "promoter" is meant a minimal sequence sufficient to direct transcription. Promoter elements that are sufficient to render promoter-

20   dependent gene expression controllable for cell type-specific, tissue-specific, temporal-specific, or inducible by external signals or agents can also be used in the invention; such elements can be located in the 5' or 3' or intron sequence regions of the native gene.

By "operably linked" is meant that a gene and one or more

25   regulatory sequences are connected in such a way as to permit gene expression when the appropriate molecules (*e.g.*, transcriptional activator proteins) are bound to the regulatory sequences.

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By "expression vector" is meant a genetically engineered plasmid or virus, derived from, for example, a bacteriophage, adenovirus, retrovirus, poxvirus, herpesvirus, or artificial chromosome, that is used to transfer a peptide or polypeptide coding sequence (*e.g.*, a TAA (*e.g.*, hTERT) peptide

5   coding sequence), operably linked to a promoter, into a host cell, such that the encoded peptide or polypeptide is expressed within the host cell.

Other features and advantages of the invention will be apparent from the drawings, following detailed description, and the claims.

Brief Description of the Drawings

10   Fig. 1A is an autoradiogram of an RNase protection assay showing expression of hTERT in U20S osteosarcoma cells infected with a retroviral rector encoding hTERT.

Fig. 1B is an autoradiogram showing telomerase activity in U20S cells expressing hTERT.

15   Figs. 2A and 2B are a pair of graphs showing hTERT-specific, HLA-restricted CTL-mediated lysis of U20S cells expressing hTERT, and inhibition, using an anti-HLA antibody, of hTERT-specific, HLA-restricted CTL-mediated lysis of U205 cells expressing hTERT.

Fig. 3A is an autoradiogram showing telomerase activity in tumor

20   cell lines.

Figs. 3B-3E is a series of graphs showing hTERT-specific, HLA-restricted CTL-mediated lysis of carcinoma (3B), multiple myeloma (3C), malignant melanoma (3D), and EBV-transformed B cell (3E) cell lines.

Fig. 4A is an autoradiogram showing the level of telomerase activity

25   in U2OS-TERT cells, NHL from two patients, and AML from one patient.

Fig. 4B is a graph showing that I540-specific CTL lysed NHL and

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AML cells in an HLA-A*201-restricted fashion

Fig. 5A is an autoradiogram showing the level of telomerase activity in U2OS-hTERT cells, patient-derived, CD34-enriched, peripheral blood cells, CD40-activated B cells, and dendritic cells.

5   Fig. 5B is a graph showing that certain normal hTERT-expressing cells are not lysed by I540-specific CTLs.

Fig. 6 are graphs showing peptide specificity of HLA-A3 restricted CTL.

Fig.7 are graphs showing that K973 CTL kill hTERT$^+$ tumors in an

10   HLA-A3-restricted fashion.

Fig. 8 is a graph showing *ex vivo* expansion of I540 CTL from a cancer patient and a healthy donor.

Fig. 9 is a series of panels showing the results of tetramer analysis of donor and cancer patient samples for I540 CTLs.

15   Detailed Description

We have discovered that the catalytic subunit of human telomerase, hTERT, includes peptides that bind HLA class I molecules. Antigen presenting cells (APCs) that present such peptides on their surfaces, in complexes with HLA, can activate cytotoxic T lymphocytes (CTLs) to specifically lyse cells

20   expressing hTERT, in an MHC-restricted fashion. The invention thus provides methods for immunotherapeutic targeting of hTERT expressing cells, such as cancer cells.

The also invention provides (i) methods of identifying and characterizing universal tumor associated antigens (TAAs), (ii) methods of

25   using such antigens (*e.g.*, the telomerase catalytic subunit, hTERT), and MHC-binding peptides of these antigens, in the prevention or treatment of cancer and

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other conditions characterized by excessive cell proliferation, and (iii) methods
of monitoring the efficacy of such prevention and treatment methods.

I. Methods of Identifying and Characterizing Universal Tumor Associated
Antigens (TAAs)

5   As is mentioned above, there is now compelling evidence in murine
model systems and in humans that immunotherapy can be used to induce
immune responses against cancer. The role of major compartments of the
immune system in such anti-tumor responses has been studied in great detail
(Rosenberg, Immunity 10:281-287, 1999). Cellular and molecular interactions
10   during the induction (priming), amplification (expansion), and effector phases
of an anti-tumor immune response have been elucidated. The identification of
genes encoding tumor associated antigens recognized by T and B cells has
given cancer immunotherapy a molecular basis (Boon et al., Annual Review of
Immunology 12:337-365, 1994; Sahin et al., Curr. Opin. Immunol. 9:709-716,
15   1997). Moreover, with the identification of the dendritic cell (DC) as the most
prominent antigen presenting cell (APC), a novel cellular adjuvant has been
introduced into the armamentarium of immunotherapy.

              However, despite these developments, there have been several
important obstacles in cancer immunotherapy, prior to the present invention.
20   For example, prior to the present invention, TAAs have been identified by
analyzing ongoing immune responses in cancer patients, yet the immune
systems of such patients are unable to regress their tumors. Moreover, most
TAA-derived peptides, prior to those identified in the present invention, bind
with low affinity, at best, to major histocompatibility (MHC) molecules, and
25   therapeutic strategies have thus required the design of derivatives with better
binding characteristics. In addition, most TAAs known prior to the present

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invention are expressed heterogeneously, limited to one or a few tumor types

and to a fraction of patients with these types of tumors (Rosenberg, Immunity

10:281-287, 1999). Due to these facts, clinical studies have been limited, as

strategies have been tested one malignancy at a time, and, in some cases (such

5   as the idiotype in lymphoma), patient by patient (Hsu *et al.*, Blood 89:3129-35,

1997). Finally, as has already been demonstrated, targeting a single tumor

antigen can lead to immunoselection of antigen loss variants (Jager *et al.*, Int. J.

Cancer 71:142-147, 1997). Similar to chemotherapy, single agent strategies in

immunotherapy may be of limited value.

10   In light of these limitations, a central hypothesis of the present

invention is that targeting a set of homogenously expressed universal tumor

antigens that contain T cell epitopes with high affinity to MHC, such that

clinically sufficient anti-tumor T cell responses are elicited by use of such

antigens, will facilitate the development of widely applicable immunotherapy,

15   circumventing immunological escape mechanisms. The methods of the present

invention allow accomplishment of these goals.

       The invention thus provides methods of identifying and

characterizing universal tumor associated antigens (TAAs). Such antigens: (1)

are expressed by the vast majority of human cancers, (2) include peptide

20   sequences that bind strongly to MHC molecules, (3) are processed by tumor

cells such that antigen-derived peptides are available for binding to MHC

molecules, and (4) are recognized by the T cell repertoire in an MHC-restricted

fashion, permitting the expansion of cytotoxic T cells (CTL) bearing specific T

cell receptors. The present invention allows the identification and

25   characterization of such tumor antigens by:

       1. using bioinformatics tools to facilitate the identification of

universal tumor antigens containing T cell epitopes with high binding affinity;

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2. establishing a time-resolved fluorometry-based assay to
simultaneously measure MHC class I binding affinity and MHC/peptide
complex stability for a large set of peptides; and

3. using a T cell screening system to facilitate the simultaneous
5   evaluation of a large set of peptides as candidate immunogenic T cell epitopes.

Using these methods, we have identified the catalytic subunit of
human telomerase (hTERT) as being a universal tumor associated antigen
(TAA). Characterization of hTERT is described further below, after a
description of our general methods.

10   *Use of bioinformatic tools in immunology*

There is clearly a very significant increase in the use of computers,
bioinformatics, and large public genetic databases in basic biology. Yet, there
remains a tremendous need to link computational sciences to other fields of
biology (Malakoff, Science 284:1742, 1999); in particular, applied biological
15   sciences, including immunology. Tumor immunology is currently
disconnected from the fast development of publicly available genetic
information, in the form of databases on the Internet, such as the Cancer
Genome Anatomy Project (CGAP) (Kuska, J. Natl. Cancer Inst. 88:1801-1803,
1996). This is rather surprising, since immunological technologies used to
20   identify TAAs are still very demanding (Boon *et al.*, Annual Review of
Immunology 12:337-365, 1994; Sahin *et al.*, Curr. Opin. Immunol. 9:709-716,
1997), and therefore the use of 'dry-lab' technologies that reduce 'wet-lab' time
in tumor immunology would greatly benefit the field. As was demonstrated for
drug development, the increase in computational power and the use of
25   computer sciences can greatly reduce the time spent for 'wet-lab'
experimentation, thereby reducing effort and cost (Larvol *et al.*, Nat.

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Biotechnol. 16(Suppl.):33-34, 1998). We have developed methods to link

tumor immunology with publicly available genetic information on cancer, thus

facilitating identification of universal TAAs (*e.g.*, hTERT; see below) and, in

particular, MHC-binding peptides of such universal TAAs.

5   *T cell mediated anti-tumor immunity*

There is considerable evidence that human T cells can specifically

lyse tumor cells (Rosenberg, Immunity 10:281-287, 1999). Most attention has

been focused on $CD8^+$ CTL as the principle effector cells of antigen-specific

anti-tumor immunity. Chief among the recent discoveries that have helped

10   propel clinical efforts has been the characterization of tumor associated

antigens (TAAs) (Boon *et al.*, Annual Review of Immunology 12:337-365,

1994). Pioneering studies in the early 1990s demonstrated the existence of

human TAAs using patients' CTLs that recognized peptides derived from these

antigens (Van Pel *et al.*, Immunological Reviews 145:229-250, 1995;

15   Rosenberg, Immunol. Today 18:175-182, 1997). Although these studies

primarily focused on melanoma, TAAs have been subsequently characterized

in several other malignancies (Van Pel *et al.*, Immunological Reviews

145:229-250, 1995; Rosenberg, Immunol. Today 18:175-182, 1997; Van den

Eynde *et al.*, Curr. Opin. Immunol. 9:684-693, 1997), raising the hypothesis

20   that most, if not all, tumors express antigens that CTL can potentially attack.

The demonstration that TAA-specific immune responses can lead to tumor

regression has been borne out extensively in animal models (Rosenberg,

Immunity 10:281-287, 1999). Although the identification of TAAs using

patients' CTLs has revitalized the field of T cell immunotherapy, the

25   methodology prior to the present invention is slow, very expensive, and

labor-intensive. Moreover, the strategy relies on the generation of

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tumor-specific T cell clones *in vitro*, suggesting that only a restricted set of

TAAs will be identified by this method. With these limitations in mind,

Pfreundschuh and colleagues developed an alternative approach, SEREX

(serological identification of antigens by recombinant expression cloning), to

5   identify TAAs (Sahin *et al.*, Curr. Opin. Immunol. 9:709-716, 1997). SEREX

makes use of patients' antibody responses to tumor-derived genes and this

strategy has accelerated the identification of TAAs significantly. Although

several T cell-defined TAAs, such as the MAGE genes, have also been

identified by SEREX, there is no information available about CTL epitopes for

10 the vast majority of genes in the SEREX database, and, of course, such epitopes

are required to activate a CTL response.

       Although there is no doubt that the identification of numerous TAAs

by CTL-based approaches or SEREX reflects the existence of an anti-tumor

immune response, it remains to be determined if these antigens play a role as

15 tumor regression antigens (Sarma *et al.*, J. Exp. Med. 189:811-820, 1999). As

is mentioned above, most T cell epitopes in TAAs identified by patient CTLs

have been demonstrated to be of low MHC binding affinity and/or low

MHC/peptide complex stability. Clinical vaccination trials have circumvented

this obstacle by utilizing altered peptides with higher MHC binding affinity and

20 higher MHC/peptide complex stability (Rosenberg *et al.*, Nat. Med. 4:321-327,

1998). This quality distinguishes TAA-derived peptides from viral peptides

that are almost exclusively of high binding affinity and high MHC/peptide

complex stability (Feltkamp *et al.*, Mol. Immunol. 31:1391-1401, 1994; Sette *et

al.*, J. Immunol. 153:5586-5592, 1994). The low binding affinity of

25 TAA-derived peptides is likely to be one of the reasons why natural CTL

responses against such peptides are not successful for tumor eradication. This

is in agreement with the finding that large numbers of TAA-specific CTLs

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co-exist with metastatic tumors in melanoma patients (Romero *et al.*, J. Exp. Med. 188:1641-1650, 1998). A recent study has even demonstrated that despite expansion, such CTLs were hyporesponsive, showing reduced cytotoxic and cytokine responses (Lee *et al.*, Nat. Med. 5:677-685, 1999).

5   To overcome these limitations of currently known TAAs, we have developed methods to identify more universal TAAs, and, in particular, those containing T cell epitopes with high MHC binding affinity and high MHC/peptide complex stability. Such TAAs and MHC-binding peptides thereof can trigger sufficient CTL responses against a broad range of tumor

10   types. Rather than analyzing tumor-derived T cell clones or tumor-specific antibodies derived from patients, an alternative strategy was used, in which TAA and their CTL epitopes are deduced from genes known to be selectively expressed in tumors. By combining bioinformatics to predict peptides that bind to HLA with high affinity, peptide binding analysis, and a powerful *in vitro* T

15   cell expansion system, the catalytic subunit of telomerase (hTERT) was identified (see below). This TAA contains at least one peptide epitope that (1) binds to HLA-A*0201 with high affinity and high MHC/peptide complex stability, (2) is naturally processed and presented by HLA-A*0201 molecules on the cell surface of a panel of tumor cell lines and fresh tumor samples, (3)

20   elicits peptide-specific HLA-restricted CTL responses, and (4) is recognized by such CTL on a wide variety of different tumor histologies. hTERT also contains at least one peptide epitope that (1) binds to HLA-A3, (2) can be used to generate HLA-A3 restricted, hTERT-specific CTL from a cancer patient, and (3) lyses tumor cells in an HLA-A3 restricted and hTERT-specific fashion (see

25   below). The identification of such CTL epitopes in hTERT demonstrates the feasibility of this approach, and provides valuable tools fro tumor immunotherapy. Also, it is desirable to identify universal tumor antigens in

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addition to hTERT to be able to target multiple TAAs, thereby circumventing immune escape mechanisms. The invention provides methods to accomplish this.

Deducing CTL epitopes in tumor associated antigens (TAAs): Making use of
5   *genomics and proteomics for tumor immunology*

Current developments in genomics and proteomics suggest that numerous TAA candidate genes can be identified. The Human Genome Project (HGP), the Human Cancer Gene Anatomy Project (CGAP), the SEREX database, and other databases, including literature databases such as PubMed,
10   provide an enormous set of data that can be analyzed to identify genes that fulfill the criteria of universal tumor antigens, as are described above. It is clear that entering the post-genomic era, none of the classical approaches to characterize TAA, including T cell cloning and testing of T cell clones against expression libraries (Boon *et al.*, Annual Review of Immunology 12:337-365,
15   1994), is suitable for the analysis of the ever-growing databases to identify a set of universal tumor antigens.

To overcome the limitations of prior methods in determining CTL epitopes, advances in bioinformatics can be applied. First, database mining and integration can be used to identify of universal tumor antigen candidates, which
20   are genes that are expressed at a much higher level in tumor cells than in normal cells. Then, computational methods are used to predict peptides derived from these proteins for high-affinity binding to MHC molecules. The requirements for peptides to bind to class I HLA molecules and to elicit CTL responses have been studied extensively (Rammensee *et al.*, Annual Review of
25   Immunology 11:213-244, 1993; Sidney *et al.*, Immunology Today 17:261-266, 1996). The strength of CD8$^+$ CTL responses depends upon the binding affinity

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of the target peptide to MHC, the peptide-MHC complex stability, and the

avidity of T cell receptor (TCR) binding for the peptide complex (Sette *et al.*, J.

Immunol. 153:5586-5592, 1994; van der Burg *et al.*, J. Immunol.

156:3308-3314, 1996; Savage *et al.*, Immunity 10:485-492, 1999; Gallimore *et*

5   *al.*, Eur. J. Immunol. 28:3301-3311, 1998). These factors directly influence the

efficiency of peptide loading and the number of peptides expressed on the cell

surface (Gallimore *et al.*, Eur. J. Immunol. 28:3301-3311, 1998). The vast

majority of viral-derived immunodominant peptides are of high binding affinity

and/or peptide-HLA complex stability (Feltkamp *et al.*, Mol. Immunol.

10   31:1391-1401, 1994; Sette *et al.*, J. Immunol. 153:5586-5592, 1994). Since

only a very small portion of peptides can bind to MHC molecules, rapid and

accurate methods to identify them, such as those used in the present invention,

can expedite the search for CTL epitopes by orders of magnitude.

A great deal of effort has been expended on the development of

15   computational methods to identify peptides that bind strongly to various MHC

alleles. It began with the work of Rammensee and colleagues, who identified

motifs in peptide sequences that serve as signatures of the MHC molecules to

which they bind (Rammensee *et al.*, Immunogenetics 41:178-228, 1995).

Motif-based methods have recently been applied to the identification of CTL

20   epitopes deduced from proteinase 3 (Molldrem *et al.*, Blood 88:2450-2457,

1996), MAGE-3 (Nijman *et al.*, Eur. J. Immunol. 23:1215-1219, 1993), MUC-1

(Brossart *et al.*, Blood 93:4309-4317, 1999), and telomerase (see below).

Typically, only 20% of peptides that carry the motif bind to the respective

MHC molecule. The inclusion of "secondary anchor" positions (Ruppert *et al.*,

25   Cell 74:929-937, 1993), the so-called extended motif, significantly improves

the specificity of motif-based methods, but they are available only for

HLA-A*0201 (Ruppert *et al.*, Cell 74:929-937, 1993) and HLA-B*3501

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(Schönbach et al., J. Immunol. 154:5951-5958, 1995). Many other statistically-based computational methods have been developed (for reviews, see, e.g., Hammer, Curr. Opin. Immunol. 7:263-269, 1995; Parker et al., Immunol. Res. 14:34-57, 1995), including the polynomial method (Gulukota et al., J. Mol.

5   Biol. 267:1258-1267, 1997), methods based on neural nets (Gulukota et al., J. Mol. Biol. 267:1258-1267, 1997; Brusic et al., Bioinformatics 14:121-130, 1998; Brusic et al., Nucleic Acids Res. 26:368-371, 1998), a method that assigns a score for each amino acid at each position as determined experimentally via single residue substitutions (Hammer et al., J. Exp. Med.

10   180:2353-2358, 1994), and a method developed by Parker et al. based on a database of the half-lives of bound β2-microglobulin (β2m) in MHC-peptide complexes (Parker et al., J. Immunol. 152:163-175, 1994). The method developed by Parker et al. assumes that the dissociation of β2m is rate-limited by the dissociation of peptide, so that variation in the microglobulin half-life

15   reflects variation in the peptide half-life. The variation is, in turn, assumed to reflect the variation in the binding affinity of the peptide. A weight matrix is then determined to best reflect the half-lives, assuming that the contribution of one peptide position does not depend on its neighboring positions. Weng and colleagues have recently developed a new statistical method (implemented as a

20   computer program named LPpep; Weng et al., http://bioinformatics.bu.edu/peptides.html) to predict strong HLA-A*0201-binding peptides. It determines the contributions for each of the 20 amino acids at each of the positions of a peptide using a linear programming algorithm. When tested on a data set of over 1000 peptides having known

25   binding affinities, LPpep has a higher sensitivity (>0.75) and specificity (> 0.9) than four other available methods.

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High volume analysis of peptide MHC affinity and MHC/peptide complex
stability

The basic principles of peptide binding to MHC molecules have been
well established in the field (Rammensee *et al.*, Annual Review of Immunology
5   11:213-244, 1993; Rothbard *et al.*, Annual Review of Immunology 9:527-565,
1991; Engelhard, Annual Review of Immunology 12:181-207, 1994; Madden,
Annual Review of Immunology 13:587-622, 1995; Pamer *et al.*, Annual
Review of Immunology 16:323-358, 1998; Rock *et al.*, Annual Review of
Immunology 17:739-779, 1999), and numerous assay systems have been
10   developed to analyze the binding of any given peptide to MHC molecules.
Binding has been analyzed using intact TAP-deficient cells (Salter *et al.*,
EMBO J. 5:943-949, 1986; Schumacher *et al.*, Cell 62:563-567, 1990) and by
in vitro assays utilizing purified HLA molecules (Ruppert *et al.*, Cell
74:929-937, 1993; Schumacher *et al.*, Cell 62:563-567, 1990; Townsend *et al.*,
15   Cell 62:285-295, 1990). While most assay systems have focused on the
maximal binding affinity, it has recently been suggested that the dissociation
rate of MHC and peptide (also measured as MHC/peptide complex stability)
may be a more important determinant for characterizing a peptide as a
dominant T cell epitope (van der Burg *et al.*, J. Immunol. 156:3308-3314,
20   1996; Busch *et al.*, J. Immunol. 160:4441-4448, 1998; Kammer *et al.*, J. Exp.
Med. 190:169-176, 1999). While cell-based assays are generally analyzed by
flow cytometry, the standard *in vitro* assays are based on competition for MHC
binding between a radioactive reference peptide and increasing concentrations
of a peptide under study. Both approaches are not ideal for high-throughput
25   screening. Only recently, a fluoroimmunoassay employing
Europium-streptavidin and time-resolved fluorometry has been described to
analyze peptide binding to murine H-2kD molecules (Jensen *et al.*, J. Immunol.

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Methods 215:71-80, 1998). We use this assay for high volume, routine
analysis of peptide binding to MHC.

In vitro analysis of CTL responses

5
The generation of antigen-specific T cells *in vitro* is a classical
immunological technique. Antigen-specific T cells can be generated relatively
easily if the peptides used to make such cells are: (1) immunodominant, (2) of
viral or other non-self origin, (3) expressed at a reasonably high copy number
on the cell surface (Porgador *et al.*, Immunity 6:715-726, 1997), and (4) of high
affinity for, and of low dissociation rate (high MHC/peptide complex stability)

10
from, MHC, and if the T cell pool under study has been exposed to the antigen
in vivo prior to *ex vivo* analysis (recall response). The frequency analysis of
peptide-specific T cells by tetramer technology (see below) revealed a
significantly higher frequency than earlier assays based on *in vitro* expansion
had suggested. It is therefore apparent that only a fraction of specific CTLs are

15
expanded in classical *in vitro* systems utilizing unstimulated peripheral blood
mononuclear cells (PBMC) as antigen presenting cells (McMichael *et al.*, J.
Exp. Med. 187:1367-1371, 1998). To circumvent these pitfalls, *in vivo* systems
utilizing transgenic mice carrying human HLA genes have been introduced
(Man *et al.*, International Immunology 7:597-605, 1995; Wentworth *et al.*,

20
International Immunology 8:651-659, 1996; Alexander *et al.*, J. Immunol.
159:4753-4761, 1997). However, these systems are expensive and are not
suitable for screening multiple peptide epitopes simultaneously. Making use of
new findings in basic immunology, it is possible to further optimize currently
available *in vitro* culture technology. The use of an APC instead of PBMC as

25
stimulators is only one example.
We have developed a system that utilizes dendritic cells (DC) for

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primary activation and CD40-activated B cells (CD40-B) for re-stimulation, thereby mimicking the physiological sequence of events between T cells and APCs during an ongoing immune response (Schultze *et al.*, J. Exp. Med. 89:1-12, 1999; Schultze *et al.*, J. Clin. Invest. 100:2757-2765, 1997). This

5   system has been successfully used for the identification of T cell epitopes derived from hTERT (see below) and the clonal immunoglobulin in B cell malignancies (see below). From a single blood draw, professional APCs, including DCs and CD40-activated B cells, are generated, and the remaining PBMCs are enriched for CD8$^+$ T cells. T cells are primarily stimulated with

10   peptide-pulsed DC, and repeatedly stimulated with peptide-pulsed CD40-B cells. Peptide-specificity and HLA-restriction is analyzed after a total of 2-5 stimulations, depending on the antigen under study. This system is not only very powerful in amplifying rare T cells against TAA-derived peptides, but has several other advantages: (1) it is relatively cheap compared to transgenic

15   mice, (2) a single blood draw is sufficient to generate all cellular components necessary, and (3) the use of professional APCs for restimulation is superior to PBMC.

Classically, the function of CTLs *in vitro* has been defined by cytotoxicity assays using radioactive chromium. Clearly, cytotoxicity analysis

20   is an important component of the characterization of a novel TAA, since tumor cell lysis is the ultimate goal of any TAA-directed immunotherapeutic intervention. However, such assays are not suitable to determine the frequency of peptide-specific CTLs. In addition, the sensitivity of cytotoxicity assays to identify very small numbers of specific CTLs is insufficient. To detect very

25   low numbers of specific CTLs and to determine their frequency, two new technologies, namely the tetramer technology (Altman *et al.*, Science 274:94-96, 1996) and cytokine ELISPOT analysis (Herr *et al.*, J. Immunol.

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Methods 203:141-152, 1997), have been developed and applied to tumor immunology. In particular, tetramers have been suggested as a tool to enrich CTL lines for peptide-specific CTL (Dunbar et al., Curr. Biol. 8:413-416, 1998; Yee et al., J. Immunol. 162:2227-2234, 1999; Valmori et al., Cancer Res.

5   59:2167-2173, 1999). Currently, the tetramer technology is still technically demanding and it is not possible to generate numerous tetramers in small quantities to screen peptide-specific CTL responses against a larger set of unknown peptides. For this purpose, cytokine ELISPOT is more suitable (Herr et al., J. Immunol. Methods 203:141-152, 1997).

10   As is noted above, technology used prior to the present invention to identify tumor antigens and peptides of these antigens that are recognized by T cells is slow, labor-intensive, and not suited for screening the large and still expanding number of potential target antigens available from HGP, CGAP, NCBI, SEREX, and other databases. To apply the vast information from

15   Genomics and Proteomics to immunotherapy, it is necessary to develop high-throughput screening systems by combining bioinformatics tools predicting immunodominant peptides, systems to efficiently screen for peptide binding, and fast and reliable T cell response analysis to screen for many potential targets simultaneously. The screening system described herein makes

20   use of the vast genetic information available in public databases, and applies this information to the identification of a set of novel universal tumor associated antigens as targets for immunotherapy of cancer. A set of universal tumor associated antigens identified in this manner can be used in widely applicable cancer immunotherapy (see below), preventing the induction of

25   immune escape mechanisms.

This screening system is not restricted to cancer, but can also be applied to infectious diseases. For example, the genetic information of a virus

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stored in a database can be analyzed for potential T cell epitopes, and these peptides can then be systematically tested in the system described here, and used in therapeutic methods, such as those described below. Moreover, the cellular system described here can form the technical platform for monitoring

5   the full dynamics of such complex immune responses as the one against cancer.

The principle of the overall approach of this invention has been established as exemplified by a universal tumor-associated antigen, hTERT, and a more restricted tumor-associated antigen, the clonal immunoglobulin of malignant B cells, which are each described further below. These data

10   demonstrate that it is possible to identify tumor antigens by combining: (1) bioinformatics for peptide prediction, (2) peptide binding analysis, and (3) a powerful *in vitro* T cell screening system (Schultze *et al.*, Journal of Clinical Investigation 100:2757-2765, 1997). Moreover, using the SEREX database that we have already established, it is possible to identify truly tumor-related

15   antigens by data mining publicly available databases.

Further details of the universal TAA identification and characterization methods are provided as below, followed by a description of how these methods were used to identify and characterize hTERT and the clonal immunoglobulin of malignant B cells.

20   *Peptide-prediction on genes in tumor-related databases: Peptide-prediction*
for MHC class I molecules

Using the SEREX database (http://www-ludwig.unil.ch/SEREX/), we assessed whether available information can be used to determine candidate genes for the proposed analysis. In July, 1999 the database contained 548 gene

25   entries. Of these sequences, full protein information was available for 245 genes (44.7%), containing approximately 140,000 9-mers and 10-mers. These

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254 genes were then analyzed for peptides predicted to bind to HLA-A*0201

using the algorithm available on the NIH Website (Parker,

http://bimas.dcrt.nih.gov/molbio/hla_bind/). Ninety-seven genes (17.7% of all

sequences in the database) were identified, with at least one peptide of

5   predicted half-life >16 hours. BLAST analyses (Altschul *et al.*, Nucleic Acids

Research 25:3389-3402, 1997) confirmed uniqueness of the sequence. Since

we want to target only genes that are cancer-related, we limited the number of

genes by data mining for information in literature databases that supported that

the gene of interest was cancer-related. Twenty-seven of these genes (4.93% of

10   all genes in the SEREX database) were already found to be associated with

cancer. A total of 49 peptides were identified from these genes were predicted

to bind with high affinity to HLA-A*0201. Conservatively calculated, the

identification of 49 prime candidate peptides out of 140,000 is a over 2000-fold

reduction of 'wet-lab' screening effort for these genes.

15   *LPpep: Further development of peptide-prediction for MHC class I binding*

A statistical method, LPpep (Weng *et al.*,

http://bioinformatics.bu.edu/peptides.html), has been developed to predict the

binding affinity of a peptide to HLA-A2, given the peptide sequence. The

binding affinities are represented as log (IC50) values, where the IC50 of a

20   ligand is the concentration required to displace 50% of a reference ligand from

a receptor. The IC50 is inversely proportional to the equilibrium binding

constant over a wide range of conditions. Like most other statistical methods,

LPpep assumes that the contribution of a given peptide side chain to binding

depends only on its position in the sequence, and is independent of its

25   neighbors. The residue contributions to log(IC50) were obtained using a linear

programming algorithm such that the cumulated absolute error between

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calculated and measured log(IC50) values was minimal. A database of 536

peptides (9-mers) and 457 peptides (10-mers) with their associated IC50 values

(measured by Sette and colleagues) with respect to HLA-A2 were used during

the analysis.

5   The ultimate goal was to select peptides that can elicit CTL

responses. Even though a peptide must first bind to an MHC molecule to elicit

a T cell response, the correlation between binding and stimulation is not

perfect. Sette and colleagues have shown that most of the peptides that can

elicit CTL responses have IC50 < 500 nM, with smaller IC50 correlated with

10   higher immunogenicity (Ruppert *et al.*, Cell 74:929-937, 1993). We therefore

confined testing of our algorithm to the most relevant immunological range,

testing performance by determining sensitivity and specificity for the selection

of: (1) strong binders (IC50 50 nM), and (2) strong and intermediate binders

(IC50 500 nM). Specifically, using 50 nM or 500 nM as cutoff, we calculated

15   the sensitivities and specificities of LPpep and four other methods on the same

data set: EM - the extended motif method (Ruppert *et al.*, Cell 74:929-937,

1993), PAR - the method by Parker *et al.* (J. Immunol. 152:163-175, 1994), PM

- the polynomial method (Gulukota *et al.*, J. Mol. Biol. 267:1258-1267, 1997),

and NN - a neural network method (Gulukota *et al.*, J. Mol. Biol.

20   267:1258-1267, 1997). For EM, PAR, and PM, we simply adopted the

parameters developed by other groups and tested them on our database. For

NN and LPpep, we developed the parameters on one part of the database and

tested them on the other part using a jackknife technique.

        The sensitivities and specificities of all five methods were

25   determined for 9-mers and 10-mers. The coefficients for 10-mers are not

available for PM, therefore, only four methods were tested for 10mers. EM

stands out as the method with the highest sensitivity and the lowest specificity.

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PM and PAR are at the other extreme: they have sensitivities close to zero and specificities close to one. LPpep and NN are the two best performers, with LPpep better than NN in terms of both sensitivities and specificities, for both cutoffs, and for both 9-mers and 10-mers.

When the 50 nM cutoff was used, LPpep has sensitivities of 0.58 (for 9-mers) and 0.71 (for 10-mers) and a specificity of 0.97. Although the sensitivities are not as high as those of EM, they are higher than all other methods. When the 500 nM cutoff was used, LPpep achieves the highest sensitivities among all methods (0.78 for 9-mers and 0.76 for 10-mers), while still maintaining competitively high specificities (0.89 for 9-mers and 0.92 for 10-mers). More interestingly, LPpep and NN seem to pick out somewhat different populations of binders. If we combine these two methods with a logical OR, i.e., a peptide is predicted to be a binder if it is predicted to be a binder by either LPpep, NN, or both, the sensitivities are substantially improved and the specificities are still high. The average absolute errors made by the three methods (PM, PAR, and LPpep) that predict log (IC50) have been compared, and LPpep has been found to have the smallest errors.

Binding of peptides to HLA molecules and stability in complexes with peptides:
Peptide-binding to HLA-A*0201 molecules using TAP-deficient T2 cells

To measure peptide binding of peptides to MHC class I molecules, as well as their stability in complexes with peptides, we employed a cellular assay using TAP-deficient T2 cells (see below). Briefly, T2 cells were incubated with peptide in serum-free medium for up to 18 hours, harvested, and subsequently stained with FITC-labeled anti-HLA-A2 mAb BB7.2 (maximum peptide binding). Increase in fluorescence intensity was determined as a function of peptide binding. For analysis of MHC/peptide complex stability,

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T2 cells were cultured for an additional 2, 4, 6, and 24 hours, and subsequently analyzed for HLA-A2 expression by flow cytometry. A MAGE-3-derived peptide that induced CTL responses in the majority of all normal donors demonstrated high binding affinity and high MHC/peptide complex stability.

5   Our data support the concept that MHC/peptide complex stability may be a more important factor than binding affinity for the likelihood to generate peptide-specific CTL responses.

A cell-lysate based ELISA to determine peptide-binding to HLA-A*0201

Microtiter plate based non-radioactive assays are best suited to

10   analyze a greater set of peptides simultaneously for MHC binding. Such an assay was adapted for the analysis of peptide-MHC binding and MHC/peptide complex stability. In addition, cellular MHC was used as a source of MHC molecules, since this circumvented the need for purification of multiple different MHC molecules. We have developed an ELISA that measures

15   MHC/peptide complexes in cell lysates from T2 cells pre-incubated with peptides. MHC/peptide complexes were detected by a conformation specific anti-HLA-A2 mAb (BB7.2) that was coated onto ELISA plates. As capture antibody of this sandwich-ELISA, we used anti-β2 microglobulin-HRP conjugates (see below). We have shown that it is possible to quantify the

20   number of MHC/peptide complexes after addition of exogenous peptide. At dilutions of up to 1:16, cell lysates derived from T2 cells pulsed with either hTERT I540 or HTLV-tax demonstrated a 2-4 fold increase over background. These data are highly comparable with results obtained in classical T2 binding assays. This assay forms the platform for MHC binding and MHC/peptide

25   complex stability assays described below.

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Peptide-binding to other HLA class I molecules using HLA-transfected T2 cells

To extend the use of this assay to other HLA-alleles,

HLA-A*0301-transfected T2 cells were evaluated in binding assays using

peptides well known to bind to HLA-A3, and the number of such complexes

5   were quantified. Furthermore, cDNAs encoding for HLA-A*0101, A*2402

have been cloned from PBMC serotyped for HLA, and subcloned into

retroviral vectors to be used in an assay to quantify the complexes.

Analysis of T cell responses in vitro

Since radioactive chromium-release assays are not suitable for

10   screening numerous CTL lines simultaneously, we have adapted several other

techniques that are suitable as read out systems for T cell screening system.

Some of the currently state-of-the-art assays include T cell analysis assays,

including non-radioactive cytotoxicity assays, cytokine ELISPOT analysis, and

tetramers.

15   *Non-radioactive cytotoxicity assay*

Utilizing time-resolved fluorometry and Europium as fluorochrome,

it has been demonstrated that chromium-release assays can be replaced by this

non-radioactive assay (Bohlen *et al.*, Journal of Immunological Methods

173:55-62, 1994). Briefly, instead of radioactively labeling target cells with

20   chromium, the cells are labeled with a Europium ligand that is released

similarly to chromium if the cells are lysed. Chelation of Europium by its

ligand leads to light emission that can be detected by time-resolved fluorometry

using a fluorometer. We have evaluated this assay using a CTL line generated

against the HLA-A3 restricted influenza A derived peptide NP265.

25   Cytotoxicity determined by Europium in a 2 hour assay was found to be even

-37-

superior to the standard 4 hour chromium release assay.

ELISPOT assay

A better estimate of the frequency of functional antigen-specific T

cells was established by the ELISPOT technique (Herr *et al.*, J. Immunol.

5   Methods 203:141-152, 1997). This assay analyses the peptide-specific CTL

response against the influenza A matrix protein derived peptide GILGFVFTL

in peripheral blood of normal HLA-A*0201 donors. Briefly, 96-well plates

lined with polyvinylidene fluoride (PVDF) membranes were pre-coated with

anti-IFN-γ mAbs to capture secreted cytokine. T cells and APC were cultured

10   onto these plates in the presence of the peptide under study. The APCs took up

and presented peptide to antigen specific T cells, inducing them to secrete

IFN-γ. After 24 hours, plates were washed, incubated with matched

biotinylated anti-IFN-γ mAbs, and an alkaline phosphatase colorimetric

reaction was induced. Resulting "spots" represented areas of T cell IFN-γ

15   secretion, while control wells (media alone or a control peptides derived from

HTLV-1 (tax)) did not induce measurable "spots." An automated ELISPOT

reader (ImmunoSpot, RTI, Inc.) was used for automated analysis.

MHC/peptide tetrameric complexes

The tetramer technology has been demonstrated to be the most useful

20   to directly enumerate peptide-specific CTL or to enrich peptide-specific CTL in

ex vivo culture systems (Lee *et al.*, Nat. Med. 5:677-685, 1999; Savage *et al.*,

Immunity 10:485-492, 1999; Altman *et al.*, Science 274:94-96, 1996; Yee *et*

al., J. Immunol. 162:2227-2234, 1999; Valmori *et al.*, Cancer Res.

59:2167-2173, 1999). We have generated tetramers composed of recombinant

25   HLA-A*0201, β2m, and a peptide derived from the HPV protein E7 or the

-38-

HTLV-1 tax protein. Using these reagents, we have been able to detect a small

fraction of E7-peptide specific T cells in a CTL line generated from peripheral

blood T cells of a normal donor by primary *in vitro* stimulation using

peptide-pulsed DC followed by two restimulations using peptide-pulsed

5   CD40-B cells. We have used tetramers to demonstrate the expansion of

hTERT-specific CTL in our T cell expansion system. These data further

confirm the peptide-specificity as functionally determined by chromium release

assays. These methods are described in further detail, as follows.

The overall aim of this invention is to develop a system that

10 facilitates the identification of novel universal tumor antigens containing T cell

epitopes of high binding affinity to MHC. By introducing bioinformatics tools,

the enormous time that would be necessary to determine such genes by

classical 'wet-lab' technology can be considerably shortened. Mining available

public databases (*e.g.*, HGP, SEREX, CGAP, and PubMed) candidate universal

15 TAA genes are identified and screened for HLA-binding motifs using

predictive computational algorithms. Peptide-prediction is followed by

HLA-binding assays. To develop an HLA-binding assay with high-throughput

capacity, several assay systems were compared using an array of peptides

available in our laboratory. Using a set of peptides from TAA currently under

20 study in the laboratory, our CTL screening system was further developed and

optimized. As read-out systems for peptide-specific T cells generated in our T

cell system, state-of-the-art T cell analysis tools were evaluated, including

non-radioactive cytotoxicity assays, ELISPOT, and tetramer technology. To

enable automation in the future, all assays involved in this system were

25 developed in micro-titer plate format.

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Bioinformatics tools to facilitate the identification of universal tumor antigens containing T cell epitopes with high binding affinity: Identifying tumor-associated antigens by data mining

To identify tumor-associated antigens, databases including, but not

5   limited to, the following can be mined: (1) CGAP (Cancer Genome Anatomy Project; http://www.ncbi.nlm.nih.gov/ncicgap/), which includes genes that are expressed only in tumors and that can be identified by comparison of the expression profiles of malignant tissue vs. normal tissue; (2) SEREX (http://www-ludwig.unil.ch/SEREX/), which is a repository of expressed genes

10 against which antibodies in the serum, from cancer patients, show reactivity; (3) HGP at NCBI (http://www.ncbi.nlm.nih.gov/genome/guide/), which includes all available human genes and ESTs and their expression information; and (4) PubMed at NCBI (http://www.ncbi.nlm.nih.gov/PubMed/), which is a database of published articles. Computational algorithms are used to search

15 CGAP, SEREX, and HGP regularly for tumor-related genes and/or gene variants, as well as their expression levels both in tumor cells and normal cells. A web-based in-house database (called TAADB) is used to store search results. Sometimes, newly discovered TAAs as reported in PubMed articles are not in CGAP, SEREX, or HGP. The appropriate information can be manually

20 extracted from the articles and store it in TAADB. TAADB integrates information on the same gene from all databases, with cross-references to the appropriate source. All genes in TAADB can be ranked according to how exclusively they are expressed in tumor cells compared to normal cells, and a higher "exclusiveness score" indicates a better candidate for a universal tumor

25 antigen.

Identifying TAA peptides that bind to major class I MHC molecules

We focused on the most common alleles (Gulukota *et al.*, Genet.

-40-

Anal. 13:81-86, 1996) - A2, A1, A3, and A24. Moreover, HLA-A3 shares

peptide specificities with A11, A31, A33, and A68, the so-called "HLA-A3

supertype" (Sidney *et al.*, Immunology Today 17:261-266, 1996). The above

four alleles combined can cover over 90% of the human population. Candidate

5   TAAs identified above and stored in TAADB were subjected to currently

available computational algorithms to predict peptides that can bind strongly to

these four MHC alleles.

Peptide prediction methods, including, but not limited to, the

following, can be used. The method developed by Parker *et al.* (J. Immunol.

10   152:163-175, 1994) is available via WWW

(http://bimas.dcrt.nih.gov/molbio/hla_bind). This method is available for all

four major HLA alleles, although we suspect the method to be the most

accurate for A2, since more experimental data are available for peptides

binding to this allele. In our previous analysis (hTERT and Ig of malignant B

15   cells, see below), we have used a cellular binding assay to test peptides

predicted by the Parker method and observed a statistically significant

correlation between the prediction and experiment. Specifically, we found this

method to have very high specificity, however relatively low sensitivity. We

have established a local version of the Parker algorithm so that all TAA

20   candidates in TAADB can be examined in minutes.

The second method is the LPpep method developed by Weng and her

colleagues, currently available on the web

(http://bioinformatics.bu.edu/peptides.html). This method has been shown by

Weng and colleagues to perform better than the Parker method (Parker *et al.*, J.

25   Immunol. 152:163-175, 1994) on a set of 1000 peptides whose IC50s have

been measured by Sette and colleagues. One obvious advantage of this method

over the Parker method is its higher sensitivity and the other advantage being

-41-

that we can further develop this method by incorporating new binding data generated using the methods described herein (see below). LPpep is currently available only for A2 and we can extend it for the other three common alleles A1, A3, and A24 (see below).

5   The third method is the neural network algorithm (NN) (Gulukota *et al.*, J. Mol. Biol. 267:1258-1267, 1997). One advantage of NN over the Parker method and LPpep is that NN does not assume that neighboring peptide positions contribute independently to the binding. We discovered that the combination of NN and LPpep could result in some overall improvement. We

10   can further develop this algorithm with new binding data generated in this project. NN is currently available for A2 and can be extended to the other three alleles (see below).

All of the above-described 3 methods were applied to the candidate TAAs identified, as is described above. There is a tradeoff between the number

15   of peptides we wanted to test experimentally and the false negative rate we were willing to tolerate. For TAAs with high exclusiveness scores, we adjusted computational methods towards high sensitivity and sacrificed some specificity. Predicted peptides were examined by sequence alignment methods (such as BLAST (Altschul *et al.*, Nucleic Acids Research 25:3389-3402,

20   1997)) to ensure that they were not related to any genes expressed in normal tissue. Peptides from multiple TAAs received high priority. Predicted peptides for all TAAs were also stored in TAADB with cross-references to the corresponding TAA. The most promising peptides were examined for MHC binding and CTL responses, as is described below. Finally, of course, other

25   similar methods can be used to identify TAAs.

As is noted above, LPpep and NN can be expanded to the other 3 major HLA alleles: A1, A3, and A24. Sette and colleagues have measured the

-42-

IC50s for a few hundred peptides binding to these 3 alleles (see, *e.g.*, Kubo *et al.*, Journal of Immunology 152:3913-3924, 1994) and this information can be used to develop residue contributions to the binding in LPpep and to train the neural network in NN. Also, two databases are publicly available that include

5   peptide sequences known to bind MHC molecules: SYFPEITHI (Rammensee *et al.*, "SYFPEITHI: An Internet Database for MHC Ligands and Peptide Motifs") and MHCPEP (Brusic *et al.*, Nucleic Acids Res. 26:368-371, 1998). However, quantitative information is not available on binding affinities, and therefore they can only be used to develop NN. Our group has accumulated

10   data from >60 peptides that have been analyzed for binding affinity, MHC/peptide complex stability, and immunogenicity using cellular assays. This pool of peptides is continuously increasing with a predicted set of 50-100 new peptides per year. The influx of binding data generated in this project can be used to further modify LPpep and NN, allowing us to restrict cellular

15   analysis to those peptides that are most likely to be recognized by T cells. LPpep can be further modified by relaxing the assumption that neighboring peptide positions contribute independently to the binding. We have explicitly incorporated a set of contributions corresponding to combinations of amino acid types at neighboring positions. Our results show that the performance of

20   LPpep can be changed by considering pairwise correlations between positions 1 and 3, 3 and 4, and 5 and 6.

Algorithms for prediction of MHC/peptide complex stability and immunogenicity

        A number of groups (van der Burg *et al.*, J. Immunol.

25   156:3308-3314, 1996; Savage *et al.*, Immunity 10:485-492, 1999; Gallimore *et al.*, J. Exp. Med. 187:1647-1657, 1998) have shown that dissociation rate is a

-43-

better predictor for immunodominance than binding affinity. Our results also

support such finding. Currently, LPpep and NN are developed based on IC50s,

which are very good estimates of equilibrium binding constants. Since using

the methods described herein, we have accumulated binding affinity and

5   dissociation rate measurements for up to 500 new peptides, and we can

establish LPpep and NN to predict dissociation rates. Among peptides with

similar binding affinities, the ones with slower dissociation rates are obviously

better choices for CTL activation.

Development of algorithms for prediction of immunogenicity

10   Moreover, according to the present invention, we have developed

computational algorithms to predict the immunogenicity. This appears to be

much more difficult than predicting binding affinities and dissociation rates,

since numerous other variables account for immunogenicity including for

example peptide processing, T cell repertoire, and co-stimulatory molecules.

15   However, we believe that there are common characteristics for immunogenic

peptides. For example, earlier studies indicated correlations between

immunogenicity and periodicity in hydrophobic residues (DeLisi *et al.*, Proc.

Natl. Acad. Sci. USA 82:7048-7052, 1985; Cornette *et al.*, Proc. Natl. Acad.

Sci. USA 92:8368-8372, 1995; de Groot *et al.*, Proteins 29:240-251, 1997).

20   Algorithms such as neural network and hidden Markov model are ideal for

recognizing subtle patterns. We have applied them to the immunogenicity

information for the peptides that we have generated, as well as over 100 T cell

epitopes in the "SYFPEITHI" database (Rammensee *et al.*, "SYFPEITHI: An

Internet Database for MHC Ligands and Peptide Motifs").

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Establishing a time-resolved fluorometry-based assay to simultaneously measure MHC class I binding affinity and MHC/peptide complex stability of a large set of peptides

We describe here a: (1) time-resolved fluorometry-based, (2)
5   micro-titer plate based, (3) relatively inexpensive, (4) but highly sensitive and
specific, assay that facilitates the analysis of numerous peptides for MHC
binding affinity and MHC/peptide complex stability. As has been shown for
murine MHC class I and II molecules (Jensen *et al.*, J. Immunol. Methods
215:71-80, 1998; Tompkins *et al.*, J. Immunol. Methods 163:209-216, 1993),
10   binding analysis based on time-resolved fluorometry using Europium as
fluorochrome fulfills these criteria. Our assay system has allowed high
throughput screening of MHC binding affinity and MHC/peptide complex
stability. The assay system is characterized by using a panel of peptides
already established and characterized in our laboratory. These peptides (n=60)
15   are restricted to HLA-A2 and -A3 and were derived from hTERT, the clonal
immunoglobulin of malignant B cells, MAGE-3, Influenza A, or HIV proteins.
A panel of new peptides identified above can then be used in the system. We
began with peptides identified from the SEREX database (n=49), followed by
universal tumor antigens identified by data mining.

20   *T2 cellular binding assay as reference assay*

The classical T2 cellular binding assay was used as a reference assay
to compare previously generated data with the new assay systems. Briefly, T2
cells were incubated with peptide in the presence of β2m in serum free medium
for 12-18 hours. T2 cells were subsequently washed and stained with the
25   BB7.2 mAb directly conjugated to FITC to determine binding affinity. Binding
was determined by the relative shift of the mean fluorescence intensity (MFI)
described as fluorescence index FI = {MFI(T2 cells plus peptide)/MFI(T2 cells

-45-

without peptide)} - 1. To measure MHC/peptide complex stability, T2 cells

were washed and kept in serum free medium until staining with BB7.2 mAb.

The analysis was performed 0, 2, 4, 6, and 24 hours after the removal of

exogenous peptide. The dissociation rate (t(MFImax/2)) is described as the

5   time with half-maximal MFI (MFI(t=0)/2).

Generation of T2 assays analyzing other HLA-alleles

        To obtain broad population coverage, the T2-based assays were

extended by transfecting additional HLA-types into these cells.

Complementary DNAs encoding HLA-A*0101, A*2402 have been cloned into

10   retroviral vectors and were used to transfect T2 cells. These HLA-types

together cover greater 90% of the whole population. A retroviral vector,

pMXpuro, harboring either of the HLA-A cDNAs was transfected into an

amphotropic packaging cell line, 293GPG, by lipofection. After 3 days, the

culture supernatant was harvested, passed through 0.45 µm filters, and then

15   used as a replication-defective retrovirus stock. For infection, T2 cells were

cultured with the retrovirus for 8-12 hours in the presence of 8 µg/ml of

polybrene, and then fresh RPMI-1640 medium was supplemented with 10%

FCS. Forty-eight hours after infection, 3 µg/ml of puromycin was added, and

drug-resistant cell lines were selected and subcloned by FACS. The different

20   T2-transfectants were standardized by the classical T2 assay procedure using

HIV-derived peptides known to bind with high binding affinity to these

HLA-types.

Direct detection of MHC/peptide complexes by ELISA

        An ELISA-based assay using T2 cell-derived cell lysates as source of

25   HLA-A2 molecules was used to measure peptide/MHC affinity and

-46-

MHC/peptide complex stability. This assay relies on the ability of exogenous

peptide to stabilize empty HLA class I molecules *in vitro* (Schumacher *et al.*,

Cell 62:563-567, 1990). T2 cells were incubated in microtiter plates with 10

µg/ml specific or irrelevant peptide for 18 hours at 37°C. Cells were lysed at

5   4°C and lysates subsequently warmed to 37°C (1 hour) for further enrichment

of correctly folded MHC/peptide complexes. Cell lysates were subsequently

transferred to ELISA plates coated with BB7.2 mAb, an antibody that only

recognizes HLA-A*0201 complexed with peptide. As a secondary reagent,

anti-β2m-HRP conjugates were used. In this case, TMB was used as substrate

10   for HRP and the reaction stopped with 1N HCL. Alternatively, a biotinylated

anti-β2m mAb can be used as capture antibody. In this case,

Europium-streptavidin can be used to detect MHC/peptide complexes on a

time-resolved fluorometer (Wallac Victor2 multi-label reader). This read-out is

more sensitive and with a higher signal-to-noise ratio (Jensen *et al.*, J.

15   Immunol. Methods 215:71-80, 1998).

        T2-A3 cells can be used to demonstrate the applicability of this assay

for other HLA-alleles. The GAP.A3 mAb is specific for peptide-complexed

HLA-A3 and does not bind endogenous T2 HLA alleles -A2 or -B5. To

determine MHC/peptide complex stability (MBAt=0/2), cell lysates are

20   incubated at 37°C in the absence of exogenous peptide for 2, 4, and 6 hours

before the ELISA is performed.

Competition assay to detect MHC/peptide complexes by ELISA

        To date, most data used for the generation of peptide-prediction

algorithms have been generated with competition assays using a radioactive

25   reference peptide and increasing concentrations of the peptide of interest

(Ruppert *et al.*, Cell 74:929-937, 1993). We have detected discrepancies

-47-

between cellular T2 assays and published data based on competition assays. To be able to compare directly these assays and to provide most accurate data for the optimization of our peptide prediction algorithms, we used a non-radioactive competition assay and compared this assay with our cellular T2

5   assay and the direct binding assay. We used T2 cell-derived MHC and a biotinylated peptide derived from the Influenza A matrix protein (FLPSDCFPSV) as a reference peptide, which was already being used as reference peptide in a fluorochrome-based assay (Kammer et al., J. Exp. Med. 190:169-176, 1999). T2 cells were incubated in microtiter plates with 10 µg/ml

10   biotinylated reference peptide and increasing concentrations of peptide under study for 20 hours at 37°C. Cell lysates were prepared as is described above and loaded onto ELISA plates coated with HLA-A2-specific mAb BB7.2. Europium-streptavidin was used to detect MHC/reference peptide complexes. A maximum fluorescence (MF) was reached with biotinylated reference

15   peptide without competitor peptide and set to 0% inhibition. The IC50 was determined as half-maximum fluorescence (MF/2 = IC50). Conditions without reference peptide were set to 100% inhibition. This allowed calculation of percentage of binding inhibition using the formula: {1 - (MF competitor peptide - MF no peptide) / (MF reference peptide - MF no peptide)} x 100%.

20   Moreover, T2-A3 cells were tested with the biotinylated influenza A nuclear protein-derived peptide NP265 as reference peptide.

The use of CD40-activated B cells for peptide-binding analysis

Since the use of T2 cells is restricted to the HLA alleles expressed on these cells, the use of other APCs is advantageous. The use of primary APC in

25   MHC binding assays allowed us to study basically any HLA type for its binding profile. Indeed, MHC binding assays have been described for

-48-

EBV-LCL (Kammer *et al.*, J. Exp. Med. 190:169-176, 1999). Therefore, we

used CD40-B cells, since these cells can be generated more easily than

EBV-LCL. The use of autologous CD40-B cells facilitates the analysis of any

given peptide on any HLA-type, as long as conformation-specific mAbs for the

5   HLA-type under study are available. Moreover, the use of primary APC

allowed us to determine if differences in binding affinity between individual

donors existed. To prepare APCs for MHC binding assays it was necessary to

empty MHC class I molecules ("stripping"). HLA molecules were "stripped"

of peptides by mild acid treatment for 90 seconds using ice-cold citric

10   acid-Na2HPO4 buffer. Immediately thereafter, the eluted cells were buffered

with cold IMDM, washed with IMDM, and resuspended at 5×10^5 cells in

IMDM with 1 μg/ml β2m. A competition assay was performed with

biotinylated reference peptides. The biotinylated peptide (150 nM) was

incubated in the presence of different concentrations of the peptide of interest

15   in 96-well V-bottom plates. 100 μl of mild acid-treated CD40-B cells were

added to these wells. The mixture was incubated for 24 hours at 37°C in the

presence of Brefeldin A to prevent binding of endogenously processed peptides

and washed twice thereafter with PBS. We compared flow cytometry of

extracellular HLA-A2 molecules (following the procedure described under

20   above) with ELISA-based time-resolved fluorometry (following the procedure

described above).

Automation of MHC binding assays

        The methods described herein can employ microtiter plate-based

peptide-binding assays that can be automated using robotics. To facilitate such

25   methods, we focus on the use of: (1) microtiter plates, (2) small volumes, and

(3) fluorometric read-out systems (Jensen *et al.*, J. Immunol. Methods

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215:71-80, 1998). Using 384-well plates, it is possible to significantly reduce volume, reagents (and therefore cost/test), and to perform competition assays (6 conditions, duplicates) for more than 30 peptides on a single plate.

A T cell screening system to facilitate the simultaneous evaluation of a large set
5   *of peptides as candidate immunogenic T cell epitopes*

The following methods were used to, *e.g.*, shorten necessary culture time (and therefore, cost and effort) by using more sensitive and specific readout systems and by establishing less labor-intensive culture conditions. This includes the use of micro-titer plates to screen for more peptides
10   simultaneously. We have used these methods on a smaller set of peptides (n<100). It is possible to fully screen up to 50 peptides for peptide-specific CTL using PBMC from a single leukopheresis.

Generation of antigen presenting cells

We have developed a system that is based on the use of immature
15   DC for primary stimulation and CD40-B cells for restimulation (Schultze *et al.*, Journal of Clinical Investigation 100:2757-2765, 1997). This system was optimized by using assays to monitor efficiency of peptide pulsing on primary APC.

DC were generated from PBMC-derived monocytes.
20   Monocyte-enriched fractions from PBMC were obtained after sheep red blood cell rosetting. This cell fraction was cultured for 6-8 days in the presence of IL-4 (1000 IU/ml) and GM-CSF (50 ng/ml) in IMDM supplemented with human serum or plasma, insulin, glutamine, and gentamicin. Further optimization was carried out by testing a combination of CD40L and IFN-γ.
25   CD40-activated B cells were generated as previously published

-50-

(Schultze *et al.*, Journal of Clinical Investigation 100:2757-2765, 1997).

Briefly, CD40-activated B cells were generated from unfractionated PBMC by

culture on tCD40L cells in the presence of IL-4 (100 IU/ml) and CsA (5.5 x

10^{-7} M). Soluble CD40L was tested as a substitute for the transfectants. The

5   use of soluble CD40L required depletion of adherent cells, since this cell

population seemed to prevent the outgrowth of B cells from PBMC when

stimulated with sCD40L, IL-4, and CsA.

Monitoring peptide-pulsing on primary APC

Although peptide pulsing has been studied in great detail for

10   TAP-deficient cell lines, there was little known about the biology of

peptide-pulsing onto primary APC. To determine the best conditions for this

procedure, biotinylated or fluorescence conjugates of the influenza peptide and

a peptide from hTERT was synthesized. Using these reagents, we determined

maximum MHC binding of peptide and their MHC/peptide complex stability

15   by varying: (1) the time of peptide-pulsing, (2) the medium for

peptide-pulsing, (3) the concentration of exogenous β2m, (4) the temperature

during peptide-pulsing, (5) the pH during peptide-pulsing, (6) the concentration

of protease-inhibitors, and (7) the concentration of reagents blocking

intracellular protein transport (*e.g.*, Brefeldin A). These experiments were

20   performed with DC and CD40-B cells.

CTL lines and their analysis

As exemplified for hTERT and Ig see below, peptide-specific CTL

responses were evaluated after 4-5 *in vitro* stimulations by chromium release

assay. Moreover, the currently employed system is limited to testing of 6-10

25   peptides per experiment and the format of the assay is not suitable for screening

-51-

larger numbers of peptides simultaneously. This system functions as the

standard for comparison of a micro titer plate based system and the use of other

readouts including ELISPOT and tetramers. Especially ELISPOT and tetramer

analysis were tested for their suitability to reduce necessary culture time to

5   identify peptide-specific T cell responses in this *in vitro* system.

We analyzed CTL lines by ELISPOT to determine the earliest time

point allowing identification of peptide-specific T cells. The analysis was

validated by cytotoxicity analysis. We expected the sensitivity of ELISPOT

analysis to be higher than that of tetramers. Moreover, this assay is more

10   suitable as readout of a screening system. Moreover, we determined whether

tetramers can be used to shorten further the time of T cell expansion to assess

peptide-specific CTL responses. For these studies, we focused on a small set of

peptides, including the HIV gag-derived peptide SLYNTVATL, the Inf A

matrix derived peptide GILGFVFTL, and the MAGE-3 derived peptide

15   FLWGPRALV.

Non-radioactive cytotoxicity assay

We substituted chromium release assays entirely by a

non-radioactive Europium release assay using a Victor2 multi-label counter

(Wallac). Two major issues were addressed. First, we established optimal

20   conditions for all potential target cells of our tumor cell panel. In particular,

different signal-to-noise ratios may be present for different sources of target

cells, similar to chromium release assays. Therefore, signal-to-noise ratios for

all available tumor cell lines were determined and a protocol established that

covers the spectrum of all the different target cell lines. Second, we tested the

25   value of this assay as a binary readout for our micro-titer plate bases peptide

screening assay (see above). Briefly, target cells were incubated for 20-30

-52-

minutes with 10 µM BATDA ligand (which forms a fluorescent chelate with Europium; Wallac, Gaithersburg, MD) in culture medium at room temperature. Cells were washed five times in culture medium. Labeling efficiency was tested before cells were subsequently cryopreserved until use as targets in

5   cytotoxicity assays. The availability of a stock of cryopreserved BATDA-labeled tumor cells and CD40-B cells further decreases: (1) variability between different cytotoxicity assays, (2) cost, and (3) labor, and allows higher throughput of screening for cytotoxicity. After cryopreservation, cells were washed and resuspended in serum-free (SF) medium (Iscove's

10   modified Dulbecco's medium (IMDM) supplemented with 5 mg/ml bovine serum albumin (BSA; Sigma), 2 mM L-glutamine, 1.25 mM sulfinpyrazone (Sigma), and 1% penicillin/streptomycin). Where indicated, peptides were pulsed with β2m in SF medium for 60-90 minutes at 37°C. Cells were washed twice in SF CTL medium, resuspended in CTL medium (5% fetal calf serum),

15   and combined with the CTL in round bottom microtiter plates. Plates were gently centrifuged at 100 x g for 2 minutes and then incubated at 37°C for 2 hours. Finally, plates were centrifuged at 300 x g, and 10 µl/well was transferred to 100 µl of 0.3 M acetic acid, 60 mM sodium acetate, 7.5 µg/ml Europium (Aldrich, Milwaukee, WI). After incubation for 15 minutes at room

20   temperature the plate was read on a Wallac Victor2 multi-label counter. The percentage of specific lysis was calculated with the following equation: 100 x ((experimental - blank) - (spontaneous - blank))/((maximum - blank) - (spontaneous - blank)).

ELISPOT assay

25   A recently established ELISPOT assay for the detection of influenza-specific IFN-γ producing T cell in peripheral blood was adapted to

-53-

analyze peptide-specific T cells in our T cell screening system. In particular,
we tested the utility of autologous peptide-pulsed CD40-B cells as a
standardized source of APC to be used in ELISPOT analysis. The ELISPOT
assay for IFN-γ was performed on Millipore 96-well plates with

5   polyvinylidene fluoride (PVDF) membranes. Plates were prepared by
overnight incubation with cytokine capture antibody at 4°C. Plates were then
washed 6 times with PBS/1% (v/v) fetal calf serum. T cells and APC were
plated in the presence of peptide at the appropriate concentration and placed
overnight at 37°C. Plates were washed with PBS/0.05% (v/v) Tween to

10   carefully remove all cells and debris before incubation with a matched
biotinylated anti-IFN-γ mAb. Plates were then washed in PBS/0.05% (v/v)
Tween, followed by incubation with streptavidin alkaline phosphatase in PBS.
Spots corresponding to areas of secreted cytokine were visualized by
incubation with 5-bromo-4-chloro-3-indolyl phosphate and nitroblue

15   tetrazolium. Spots were quantified using an automated ELISPOT reader
(ImmunoSpotTM from RTI, Inc.), and graphical and numerical data was stored
in the TAADB database (see above).

MHC/peptide tetramers

Preliminary data suggest that between 0.5-4% of peptide-specific

20   CTL are generated in our T cell screening system. With the use of tetramers
we addressed the following questions: (1) At which time point during T cell
expansion can we detect tetramer-positive cells (given a detection limit of
0.1%)? (2) Can we identify more favorable culture conditions for the
expansion of peptide-specific CTL by monitoring the culture with tetramer?

25   (3) What is the impact of different concentrations and timing of IL-2 on the
expansion of tetramer-reactive T cells? (4) Can we expand tetramer-positive

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cells generated in our system after flow assisted cell sorting and what are the best antigen-independent culture conditions to expand these CTL?

For flow cytometric analysis of T cell populations, approximately 0.5 μg of tetramer was added to T cells for 15 minutes at room temperature in
5   PBS/3%FCS. The cells were washed twice with cold PBS/1%FCS and once with cold PBS, and then analyzed by flow cytometry. We primarily studied HLA-A2 tetramers, however, tetramers including other HLA-alleles can be studied as well.

Development of a micro titer plate-based assay system

10   To screen more peptides simultaneously, an assay based on 96-well plates was used. CD8$^+$ T cells were isolated from PBMC and primarily stimulated with autologous peptide-pulsed DC (ratio T:DC = 20:1), followed by stimulation with peptide-pulsed CD40-B cells (ratio T:CD40-B = 4-10:1). While IL-7 was added during every re-stimulation, IL-2 was started after 8
15   days of culture, and every 2-3 days thereafter. Cultures were started with at least 2.5 x 10^5 CD8$^+$ T cells/well and a minimum of 12 wells/condition. A start population of 3-4 x 10^6 CD8$^+$ T cells was sufficient to perform the analysis described here. Every 7 days the cultures were monitored for expansion by determining CD8$^+$ T cells using a Coulter counter and phenotypic analysis for
20   CD8 expression. The number of peptide-specific T cells was monitored by ELISPOT analysis. For this purpose, for every given time point, 3 wells were harvested and placed on PVDF membrane plates, and screened for IFN-γ specific CTL, as is described above. Alternatively, if tetramers are available, phenotypic analysis can be performed for a small set of peptides. If ELISPOT
25   or tetramer analysis demonstrated peptide-specific CTL until day 21, an initial cytotoxicity screen using peptide-pulsed CD40-B cells is initiated on day 25.

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We perform a single E:T ratio in the range of effector:target cells = 10-30:1. If a positive result is obtained in this screen, a second screen is initiated to test if peptide-specific CTL can kill tumor cell lines from the tumor cell panel described below.

5   *Tumor cell screening panel*

We have established a panel of tumor cell lines that allows us to determine if peptide-specific CTL recognize tumor cells of different histological origin indicating natural expression and presentation by MHC class I molecules. Furthermore, these cell lines are used to confirm HLA-restriction.

10   One of the goals of the tumor cell panel is to be able to screen CTL responses to most tumor histologies on the most widely expressed HLA types. The current panel allows the screening for HLA-A2 restricted CTL responses in a wide variety of tumor histologies. To broaden the applicability of the system to other HLA-types, the tumor cell line panel can be genetically

15   characterized for complete HLA expression.

Since we can identify genes by publicly available information, data is available for every new tumor antigen identified using our method, stating the expression of the gene of interest by tumor cells. However, to use the tumor cell line panel as a screening tool for CTL, it is necessary to determine

20   the expression of tumor antigens under study to be able to interpret results from cytotoxicity assays or cytokine release analyses.

The expression of a gene of interest can be examined on protein level. We used an already prepared bank of snap frozen samples (stored at -80°C) of all cell lines. To measure the protein of interest, cell lysates were

25   prepared using appropriate conditions. For screening purposes, Western blots were performed on mini gels. Alternatively, if monoclonal antibodies against

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the protein of interest are already available, an ELISA is performed on cellular
lysates. The expression analysis on the tumor cell line panel establishes the
method of choice that is used to screen primary tumor samples for expression.

If qualitative protein analysis is not feasible due to the lack of

5   appropriate reagents or due to low-level expression of the protein (e.g., hTERT;
see below), expression is analyzed on the RNA level. RT-PCR using
gene-specific primers is performed using standard techniques. For this
purpose, we prepared cDNA from all tumor cell lines in the panel. We
established the complete cDNA screening process using gene-specific primers

10   for MAGE-3 and MUC-1. We validated the system by screening two to three
genes identified, as is described above. The setup of the RT-PCR screen
facilitates automation of this method.

As is noted above, the methods described above for identifying
universal TAAs including peptides that bind MHC have been carried out in the

15   identification of the catalytic subunit of telomerase, hTERT. As proof of
principle, these methods have also been used to identify MHC-binding peptides
within the clonal immunoglobulin of malignant B cells, which is a tumor
antigen specific for malignant B cells (i.e., it is not a universal TAA). These
studies are described in further detail below.

20   *Framework derived peptides from clonal immunoglobulin of malignant B cells*

Most B cell malignancies are characterized by the clonal expansion
of a single B cell. Since each Id is patient specific, classical approaches (Boon
et al., Annual Review of Immunology 12:337-365, 1994) to determine
Id-derived peptides recognized by a patient's T cells are extremely difficult to

25   apply to this particular tumor antigen, and would require investigation in every
patient. To overcome this limitation, we applied the approach described above.

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A large database of Ig sequences from patients with B cell malignancies was
screened for peptides binding to HLA-A*0201 using peptide prediction
software (Parker, http://bimas.dcrt.nih.gov/molbio/hla_bind). Samples from
192 patients with B cell malignancies were analyzed. The tumor-specific Ig

5   heavy chain rearrangement was PCR amplified and directly sequenced in 128
of these patients (67%). In 35 of these patients, tumor-rearranged light chain
sequences were also obtained. The 163 Ig heavy and light chain
rearrangements were translated to their deduced amino-acid sequences. From
these sequences 794 peptides were identified with a predicted half-life of

10    $\beta 2m$-dissociation greater than one minute. From these 794 peptides, 229
(28.8%) were derived from the complementarity determining (CDR) regions of
the Ig sequences. The remaining 565 peptides (71.2%) were derived from
framework region (FR) motifs. Among the 565 FR-derived peptides, many
were shared such that only 272 different peptide sequences were identified.

15   Among these 272 peptides, 29.5% were shared by at least two patients. Peptide
binding of a total of 35 peptides, including all peptides with a predicted
half-life of binding greater than 2 hours, was performed. Overall, we found a
correlation (Spearman rho=0.61, p=0.0001) between the predicted half-life and
the ability of the peptides to bind to HLA-A*0201 as determined by the T2

20   binding assay. Utilizing our current T cell screening system, we identified ten
peptides that induced peptide-specific CTL. Sixty-seven percent of the
HLA-A2$^+$ patients (42/63) expressed at least one of the common nine
FR-derived epitopes in their malignant clonal Ig, showing that a single
Ig-derived peptide could be a relevant target in a great number of patients with

25   B cell malignancies. CTL generated against FR-3, FR-4, FR-9, FR-11, and
FR-12 demonstrated specific recognition of the parent CLL cells, but not CLL
cells that did not express the FR motifs. These results show that the CLL cells

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were capable of processing and presenting Ig-derived peptides. Specific lysis of target cells was inhibited by anti-HLA-A2 mAb, demonstrating HLA-A2 restriction. CTL generated against peptide FR-12 killed CD40-B pulsed with the corresponding peptide and tumor cells from three patients with CLL

5   expressing this peptide, but not unpulsed CD40-B cells. There was increased killing of CLL cells when they were pulsed with the relevant peptide. Similar results were obtained for peptide FR-11. CD40 activation of the CLL cells also resulted in increased efficiency of killing by the CTL.

Identification of hTERT peptides capable of binding to HLA class I antigens

10   hTERT (Genbank Accession No. AF018167) is expressed in more than 85% of human cancers. To begin evaluating the potential usefulness of hTERT as a TAA for cancer immunotherapy, we first analyzed its sequence for peptides that could potentially bind to HLA class I molecules using a peptide-motif scoring system

15   (http://bimas.dcrt.nih.gov:80/cgi-bin/molbio/ken_parker_comboform). Starting with the most common HLA subtype, HLA-A*0201, we identified and tested three candidate nonapeptides (Table 1). Each has a unique coding sequence within the currently available human genome sequence. Peptides were synthesized by Genosys Biotechnologies, Inc. (The Woodlands, Texas).

20   **Table 1.** Binding of hTERT peptides and controls to human HLA-A*0201

Name	Sequence	Protein	Position	Score*	Fluorescence Index[+]
I540	ILAKFLHWL (SEQ ID NO:1)	hTERT	aa540	1746	3.1
E555	ELLRSFFYV (SEQ ID NO:3)	hTERT	aa555	1670	2.2

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R865	RLVDDFLLV (SEQ ID NO:4)	hTERT	aa865	542	2.2
F271	FLWGPRALV (SEQ ID NO:5) (positive control)	MAGE-3	aa271	2655	2.7
1540-S	HFLLWKLIA (SEQ ID NO:6) (negative control)	hTERT	scrambled	0	0.2
A98-Id*	AHTKDGFNF (SEQ ID NO:7) (negative control)	Idiotype	aa98	0	0.0

*Calculated score in arbitrary units. †(Mean fluorescence with peptide - mean fluorescence without peptide)/(mean fluorescence without peptide). Results representative of two experiments. *Peptide sequence obtained from the idiotypic sequence of a patient with plasma cell leukemia and predicted to bind to HLA-B38.

To test the relative binding of each peptide to HLA-A*0201, 50 μg/ml of each peptide plus 5 μg/ml of β2-microglobulin were pulsed onto HLA-A*0201⁺ TAP-deficient T2 hybridoma cells (ATCC, Rockville, MD) in serum-free RPMI medium for 18 hours at 37°C. Expression of HLA-A*0201 was then measured by flow cytometry using mAb BB7.2 (ATCC) followed by incubation with FITC-conjugated F(ab')2 goat anti-mouse Ig (Zymed, South San Francisco, CA; Nijman et al., Eur. J. Immunol. 23:1215-1219, 1993). Based on significantly increased expression of HLA-A*0201 on pulsed T2 cells, each peptide was found to bind strongly to HLA-A*0201 (Table 1). A positive control peptide derived from the tumor antigen MAGE-3 also bound strongly, but two negative control peptides did not.

Generation of hTERT-specific CTLs

We then generated CD3⁺CD8⁺ CTLs specific for the hTERT peptides and tested them for their ability to kill tumor cells in an hTERT-dependent

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fashion. These CD3+CD8+ CTLs were generated as follows. Informed consent was obtained from volunteer blood donors, their peripheral blood mononuclear . cells (PBMC) were isolated by leukopheresis and Ficoll-density centrifugation, and dendritic cells (DC), CD40-activated B cells, and CD8-enriched T cells

5   were prepared from PBMC of normal HLA-A*0201 donors, as previously described (Schultze et al., J. Clin. Invest. 100:2757, 1997).

DC were prepared from PBMC depleted of T, B, and natural killer cells using IL4 and GM-CSF; >80% of these cells were CD83+ CD14-. B cells from PBMC were activated via CD40 and cultured; >80% of these cells were CD19+

10   CD3-. CD8-enriched T cells (>89% CD8+, >95% CD3+, <0.5% CD4+, and <5% CD56+) were prepared from PBMC. Flow cytometry was performed as described in Schultze, supra.

DC were harvested after 7 days in culture, pulsed with peptide (40 μg/ml) and β2-microglobulin (3 μg/ml) for 4 hours at 37°C, irradiated (33 Gy),

15   and added to autologous CD8-enriched T cells at a T:DC ratio of 20:1 in RPMI media with 10% human AB serum, 2 mM glutamine, 15 μg/ml gentamicin, 20 mM HEPES, and 10 ng/ml IL7 (Sigma, Saint Louis, Missouri). At day 7 and weekly thereafter, T cell cultures were harvested and restimulated with irradiated (33 Gy), peptide-pulsed autologous CD40-activated B cells as

20   described in Schultze, supra. IL2 (50 U/ml; Collaborative Biomedical Products, Bedford, Massachusetts) was introduced on day 8 and replenished as needed every 3-4 days. After three restimulations, 88-90% of cells in each culture were CD3+ lymphocytes, of which 88-90% were CD8+ and 0.3-3.6% were CD4+. Cultures were <0.4% CD14+ and 3.0-3.9% CD56+.

25   To create target cells in which hTERT was processed naturally, we used amphotropic retroviruses to infect the hTERT-negative, HLA-A*0201+ osteosarcoma line U2OS with either the full coding sequence of hTERT

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(U2OS-TERT cells) or with retroviral vector alone (U2OS-pB cells). Briefly, the EcoRI-SalI fragment containing the hTERT-HA cDNA was subcloned from plasmid pCI-Neo-hTERT-HA (Counter *et al.*, Oncogene 16:1217, 1998) into the EcoRI-SalI site of pBabe-puro (Morgenstern *et al.*, Nucleic Acids Res.

5   18:3587, 1990). The carboxyl-terminal HA tag in this construct was deleted by PCR amplification of an hTERT EcoRV-SalI fragment with a primer that deleted the nucleotides encoding the HA tag. U2OS cells were infected with pBabe-puro (negative control) or pBabe-puro-hTERT retroviruses and selected in 0.5 µg/ml of puromycin. Total RNA (40 µg) was isolated from the resulting

10   polyclonal populations and assayed for hTERT expression by an RNase protection assay (Fig. 1A), as described in Counter *et al.*, *supra*. Fig. 1A shows that U2OS-TERT cells expressed hTERT mRNA, whereas U2OS-pB control cells did not. Input anti-sense probes are shown on the left of Fig. 1A, and RNase-resistant, protected fragments representing hTERT and human β-actin

15   are shown on the right.

Fig. 1B shows that U2OS-TERT cells demonstrated telomerase activity, whereas U2OS-pB cells did not. In this experiment, 0.2 µg or 0.02 µg of cytosolic cellular extracts prepared from the vector- or hTERT-infected cells was assayed for telomerase activity using a PCR-based telomerase repeat

20   amplification protocol (TRAP; Kim *et al.*, Nucleic Acids Res. 25:2595, 1997). As a negative control, 2 µg of each extract was heat treated (HT) to inactivate telomerase prior to assay.

U2OS-TERT and U2OS-pB cells expressed similar levels of HLA-A*0201 and CD58, and lacked MHC class II, CD54, and CD80.

25   Fig. 2A shows that CTLs generated by stimulation with the hTERT peptide I540 lysed only hTERT-positive cells. U2OS-TERT cells (solid symbols) and U2OS-pB cells (open symbols) were labeled with Cr^{51} and used

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as targets for I540-stimulated CTLs (squares) or MAGE-3-stimulated CTLs
(circles). Standard 4-hour Cr^{51}-release assays after the third or fourth
restimulation were performed to measure cytotoxicity. Assays were done in
triplicate per condition using 5 x 10^3 labeled target cells per well in a 96-well

5   plate, and percent specific lysis was calculated from cpm of (experimental
result - spontaneous release)/(maximum release - spontaneous release). The
mean results (± 1 S.D.) of one experiment, representative of three performed,
are shown. I540-stimulated CTLs killed only U2OS-TERT cells. In contrast,
CTL cultures generated by stimulation with the other two candidate hTERT

10   peptides or with the MAGE-3 peptide did not lyse either U2OS-TERT cells or
U2OS-pB cells (Fig. 2A).

       Fig. 2B shows that the lysis of hTERT-positive cells by I540-specific
CTLs is HLA class I-restricted. I540-specific cytotoxicity against
U2OS-TERT cells was tested at an effector:target ratio of 30:1. Consistent

15   with HLA-restricted cytotoxicity, lysis of U2OS-TERT cells by I540-specific
CTLs was inhibited by the anti-HLA-A2 mAb BB7.2, but not with media or the
anti-B5 control mAb. The results shown in Figs. 2A and 2B strongly suggest
that the I540 hTERT peptide fulfills the requirements for a TAA capable of
triggering CTL responses: the peptide is naturally processed by tumor cells,

20   presented in an MHC-restricted fashion, and permits expansion of
hTERT-specific CTLs.

I540-specific CTLs recognize tumor cell lines that express hTERT

       To test whether I540-specific CTLs can recognize hTERT in a broad
range of tumors, cytotoxicity was evaluated against a panel of tumor cells with

25   diverse histologic origins. The 36M ovarian carcinoma cell line generated from
patient ascites was a gift of Dr. Stephen Cannistra, Dana-Farber Cancer

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Institute. The EBV-transformed B cell line B4 (Counter *et al.*, J. Virol. 68:3410, 1994) was provided by Dr. Chris Counter, Duke University. The transformed kidney cell line 293, the lung carcinoma line Calu-1, the multiple myeloma cell lines U266, IM9, and HS-Sultan, and the EBV-transformed B

5   cell line SKW6.4 were obtained from the ATCC (Rockville, Maryland). The malignant melanoma cell lines K029 and K017, generated from biopsy specimens, were a gift of Dr. Glenn Dranoff, Dana-Farber Cancer Institute.

Cytosolic extracts were prepared from each cell line and assayed for telomerase activity as described for the experiment shown in Fig. 1B. For

10   Calu-1, B4, K029, and K017, 1 μg of extract was used in the assay. For each other cell line, 200 ng of cytosolic extract was used, except 293 cells (positive control), for which 30 ng was used. Telomerase activity was observed in all tumors except one melanoma cell line (Fig. 3A). The TRAP internal control (IC) is shown for each extract. HLA class I expression was determined for

15   each cell type shown in Fig. 3A by flow cytometry as described (Schultze *et al.*, J. Clin. Invest. 100:2757, 1997); each tumor cell type expressed nearly equal amounts of surface MHC class I. HLA-A*0201 typing was evaluated by serology and confirmed by PCR amplification in our institute's clinical laboratory.

20   Figs. 3B-3E are graphs showing that I540-specific CTLs lyse tumor cells from a wide variety of histologic origins in an HLA-A*0201-restricted and telomerase-dependent fashion. Figs. 3B-3E show the cytotoxicity of I540-specific CTLs against carcinoma (Fig. 3B), multiple myeloma (Fig. 3C), malignant melanoma (Fig. 3D), and EBV-transformed B cell lines (Fig. 3E).

25   Experiments were performed as described for Fig. 2. The mean results of one experiment, representative of two experiments performed, are shown ± 1 S.D. Lysis of U2OS-TERT cells is shown for comparison in each graph.

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HLA-A*0201 (A2) and telomerase (Tel) phenotypes for each target cell type

are summarized in Fig. 3A.

The I540-specific CTLs lysed an HLA-A*0201$^+$ carcinoma line, but not

an HLA-A*0201-negative carcinoma line (Fig. 3B); in contrast, CTLs

5   generated using the MAGE-3 peptide did not lyse either carcinoma line.

Similarly, the I540-specific CTLs lysed two HLA-A*0201$^+$ multiple myeloma

cell lines but not an HLA-A*0201-negative myeloma line (Fig. 3C), and also

lysed an HLA-A*0201$^+$ malignant melanoma line but not an

HLA-A*0201-negative, telomerase-negative melanoma line (Fig. 3D).

10   Finally, we tested I540-specific CTLs against Epstein Barr virus

(EBV)-transformed B cell lines as a model of EBV-related lymphoproliferative

disorders. Each of these lines expressed HLA-A*0201, but only the line

SKW6.4 was telomerase-positive; B4 is a mortal, pre-crisis line and therefore

telomerase-negative (Fig. 3A) (Counter, et al., J. Virol. 68:3410, 1994).

15   I540-specific CTLs lysed SKW6.4 but not B4 (Fig. 3E), further demonstrating

hTERT specificity of the cytotoxic response. The results shown in Figs. 3A-3E

demonstrate that in a wide range of tumors and transformed cells, endogenous

hTERT is naturally processed, presented in the context of HLA-A*0201, and

serves as a target for antigen-specific CTLs.

20   To investigate the possibility that I540-specific cytotoxicity was

restricted to immortalized cell lines, we then studied CTL lysis of freshly

isolated, primary tumor cells. Acute myelogenous leukemia (AML) cells were

obtained by bone marrow aspiration from an HLA-A*0201 patient at the time

of clinical presentation, and non-Hodgkin's lymphoma (NHL) cells from two

25   patients were obtained after biopsy of markedly involved lymph nodes. One

NHL patient expressed HLA-A*0201 (patient 1) whereas the other patient was

HLA-A*0201 negative but MHC class I-positive (patient 2). Each primary

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tumor tested was telomerase-positive (Fig. 4A). As is shown in Fig. 4B, I540-

specific CTL lysed the HLA-A*0201 AML and NHL cells, but not the HLA-

A*0201 negative NHL cells. These results demonstrate that in a range of

primary tumors and transformed cell lines, endogenous hTERT is naturally

5   processed, presented in the context of HLA-A*0201, and serves as a target for

antigen-specific CTL.

        To evaluate the relative efficiency of I540 recognition by the CTL

populations tested and hence to assess the significance of the level of

cytotoxicity obtained against telomerase positive cells, we compared

10   cytotoxicity of I540 CTL with MAGE-3 F271 CTL against the same target.

The K029 melanoma cell line was used as the target because it endogenously

expresses both hTERT and MAGE-3. Two pairs of I540-specific and F271-

specific CTL were generated (including one pair form the same donor), and

were directly compared. Over a range of E:T ratios, I540-specific and F271-

15   specific cytotoxicity against K029 was similar (*e.g.*, 46.1% versus 32.0%,

respectively, for one pair of CTL, and 87.0% versus 64.7% for a second pair of

CTL generated from the same donor, tested at an E:T ratio of 30:1). Although

this finding suggests that CTLs recognizing I540 and F271 have similar

cytotoxic efficiencies for tumor cells expressing these antigens, we are

20   currently generating a panel of T cell clones form healthy donors and cancer

patients to answer this question definitively.

Testing for hTERT autoimmunity

        Because the vast majority of human cancers have high levels of

telomerase activity, immunotherapeutic strategies aimed at this antigen

25   potentially have broad clinical applications. The major concern of such

approaches would be cytolysis of the few normal cell types in which telomerase

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is detected. Telomerase activity has not been detected in adult cardiac, renal

hepatic, pulmonary, neural, skeletal, and adipose tissues; however,

hematopoietic stem cells and progenitors (Broccoli *et al.*, Proc. Natl. Acad.

Sci. U.S.A. 92:9082, 1995; Hiyama *et al.*, J. Immunol. 155:3711, 1995;

5   Buchovich *et al.*, Mol. Bio. Cell 7:1443, 1996), germinal center cells, basal

keratinocytes, gonadal cells, and in some studies, certain proliferating epithelial

cells (Igarashi *et al.*, Blood 89:1299, 1997; Norrback *et al.*, Blood 88:222,

1996; Harle-Bachor *et al.*, Proc. Natl. Acad. Sci. U.S.A. 93:6476, 1996;

Yasumoto *et al.*, Oncogene 13:433, 1996; Weng *et al.*, Proc. Natl. Acad. Sci.

10   U.S.A. 94:10827, 1997; Kolquist *et al.*, Nat. Genet. 19:182, 1998) have

measurable telomerase activity. We therefore examined I540-specific CTL

lysis of normal cells, starting with peripheral blood CD34^{+} cells as important

potential targets. CD34-enriched cells from two patients with lung cancer were

studied (patient cells were obtained for these experiments from excess material

15   with the permission of our institution's Internal Review Board). These patients

had undergone stem cell mobilization with chemotherapy in preparation for

autologous stem cell transplantation. Cells from Patient 1 were HLA-A*0201^{+}

and 45% CD34^{+}CD45^{+}, and cells from Patient 2 were HLA-A*0201^{-} (but Class

I^{+}) and 76% CD34^{+}CD45^{+}.

20   Figs. 4A and 4B show an evaluation of I540-specific CTL cytotoxicity

against normal hematopoietic cells. In Fig. 4A, telomerase activity is shown

for U2OS-TERT cells, CD34^{+}- enriched peripheral blood cells from Patients 1

and 2, CD40-activated B cells, and DC. For U2OS-TERT cells, 300 ng or 100

ng of cytosolic extract were used; for the other cells, 1 µg or 300 ng were used.

25   As a negative control, 2 µg of each extract was heat treated (HT) to inactivate

telomerase prior to assay. The TRAP internal control (IC) is shown for each

reaction.

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In Fig. 4B, I540-specific CTLs were tested for cytotoxicity against CD34-enriched cells, autologous DC, and autologous CD40-activated B cells. Lysis of U2OS-TERT cells is shown for comparison. HLA-A*0201 (A2) and telomerase (Tel) phenotypes are summarized for each target. Experiments

5   were performed as in Fig. 2. The mean results of one experiment, representative of two performed, are shown ± 1 S.D.

Although the CD34-enriched cells of each patient had telomerase activity (Fig. 4A), no lysis by I540-specific CTLs was observed (Fig. 4B), suggesting that hTERT does not readily function as an autoantigen on

10   hematopoietic precursor cells. This finding can reflect a level of hTERT expression on CD34-enriched cells that is insufficient for CTL activation, but still sufficient for detection by the PCR-based telomerase assay (quantitative differences in hTERT expression between cell types cannot be determined by the PCR telomerase assay, although qualitative differences such as the presence

15   or absence of signal are meaningful (Prowse et al., Proc. Natl. Acad. Sci. U.S.A. 92:4818, 1995).

Assuming that hTERT expression in stem cells and progenitors is not rate-limiting for CTL activation, we hypothesized that these cells might not be recognized as hTERT-specific CTL targets because of an hTERT processing

20   defect that limits or prohibits the presentation of hTERT peptides in the groove of MHC Class I. We therefore examined the ability of I540-specific CTLs to lyse professional antigen presenting cells in which any such defect would be less likely to be present. Autologous DC prepared from peripheral blood lacked telomerase activity and were not lysed by I540-specific CTL (Figs. 4A

25   and 4B). Resting peripheral B cells also lack telomerase activity, but after prolonged stimulation in vitro with CD40 ligand, display detectable telomerase activity (Fig. 4A). CD40-activated B cells are excellent antigen presenting

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cells (Schultze *et al.*, J. Clin Invest. 100:2757, 1997) and parallel germinal

center B cells in many ways, including their telomerasc activity. As shown in

Fig. 4B, autologous CD40-activated B cells were lysed by I540-specific CTL.

Therefore, it is theoretically possible that hTERT-specific CTLs could, if given

5   therapeutically, kill germinal center B cells and other activated B cells.

However, our observation that DCs lack telomerase activity suggests that DCs

could maintain primary antigen-specific T cell activation even if exposed to

hTERT-specific CTLs.

        In an attempt to test whether other normal telomerase-positive cells are

10   susceptible to hTERT-specific lysis, we obtained freshly isolated human

foreskin keratinocytes and human oral keratinocytes and tested them for

telomerase activity. Consistent with other reports (Klingelhutz *et al.*, Mol.

Cell. Biol. 14:961-969, 1994; Klingelhutz *et al.*, Nature 380:79-82, 1996;

Stoppler *et al.*, J. Biol. Chem. 272:13332-13337, 1997; Kiyono *et al.*, Nature

15   396:84-88, 1998), we did not find that freshly isolated keratinocytes express

detectable telomerase activity (Fig. 5A). In a report that identifies telomerase-

positive keratinocytes (Harle-Bachor *et al.*, Proc. Natl. Acad. Sci. USA

93:6476-6481, 1996), the authors were only able to isolate telomerase-positive

cells through a time-sensitive, trypsin fractionation protocol from whole

20   epidermis. This protocol produced enough cells to perform the PCR-based

TRAP assay but insufficient to perform chromium-release assays. Likewise,

we have been unable to establish a primary epithelial cell culture that expresses

endogenous telomerase. Consequently, extensive *in vitro* evaluation as to

whether hTERT specific CTL would lyse normal telomerase positive cells

25   requires the ability to first obtain such cells in sufficient quantity for the

appropriate assays. Clinical attempts to target hTERT as a tumor antigen in

cancer patients also offers major insights into this question.

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In summary, we demonstrate that a peptide derived from the catalytic subunit of human telomerase can be naturally processed by tumor cells, presented in an HLA-A*0201-restricted fashion, and serve as a target for antigen specific CTL. Furthermore, cytotoxicity can be directed against target

5   cells from a wide variety of histologic origins including carcinoma, sarcoma, multiple myeloma, malignant melanoma, acute leukemia, Non-Hodgkin's Lymphoma, and EBV-transformed B cells. These findings, together with the identification of telomerase in the vast majority of human cancers, suggest that hTERT represents the most commonly-expressed TAA yet described.

10   We did not observe cytotoxicity against telomerase-positive, CD34$^+$ (telomerase-positive) peripheral blood cells. Given that more than 85% of all cancers contain hTERT-expressing tumor cells, and that nearly 50% of the population expresses the HLA-A*0201 allele, almost half of all cancer patients can benefit from immunotherapeutic strategies employing the I540 hTERT

15   peptide. The percentage of cancer patients benefitting from hTERT-specific immunotherapies can be further increased by use of additional hTERT peptides that bind to other HLA alleles.

Identification of TAA peptides that bind to histocompatibility molecules

      For the full characterization of hTERT as a widely expressed tumor

20   antigen, additional CTL epitopes derived from hTERT can be pursued. It is important in the design of hTERT-specific immunotherapies to identify multiple hTERT epitopes restricted to HLA-A*0201, as well as multiple epitopes restricted to other HLA alleles. In the case of hTERT, tumor progression is characterized by increased expression and activity of telomerase

25   (Kolquist *et al.*, Nat. Genet. 19:182-186, 1998). Nevertheless, mutations within a single epitope that do not disrupt function are at least hypothetically

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possible and could facilitate tumor resistance to clinical strategies based on a single epitope.

Numerous previous investigations have identified T cell epitopes based on the reactivity of patient-derived, tumor specific clones. An alternative

5   strategy, as is described above, is to deduce CTL epitopes from the known sequences of genes that encode candidate tumor antigens, such as hTERT. Our hypothesis behind this strategy contends that CTL epitopes can be predicted by comparing candidate protein sequences with amino acid motifs thought to be important for MHC/peptide binding. For certain HLA alleles, and in particular

10   HLA-A*0201, a great deal of empiric data on MHC/peptide binding has been utilized to delineate these motifs, leading to highly specific and moderately sensitive prediction algorithms for MHC/peptide affinities (Parker *et al.*, J. Immunol. 152:163, 1994). Binding to HLA-A*0201, for example, is favored by Leu or Met residues at anchor position 2 and by Leu and Val residues at

15   anchor position 9. Glu, Asp, or Lys residues at position 4 also favor binding to this allele.

A computer-assisted peptide-binding prediction program is available on the Internet (http://bimas.dcrt.nih.gov:80/cgi-bin/molbio/ken_parker_comboform), which, for a given allele, scores candidate

20   peptides for their estimated dissociation half life (in minutes). Numerous hTERT-derived 9mers and 10mers are predicted to bind to HLA-A*0201, and these peptides represent candidate CTL epitopes with high affinity for this allele (Table 2). Furthermore, this type of analysis also predicts binding of several other hTERT-derived peptides to non-HLA-A*0201 alleles (Table 3).

25   It has become evident that the threshold of scores that predict binding varies for each HLA allele and will be determined by analyzing scores of peptides previously shown to bind (*i.e.*, "positive controls" in Tables 2 and 3). For

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example, scores above 500 predict high-affinity binding to HLA-A*0201

whereas scores above 80 and 90 predict binding to HLA-A3. For each hTERT

peptide listed in Tables 2 and 3, initial BLAST searches indicate a unique

coding sequence within the currently available genomic database. For any

5   given patient, therefore, it is possible to assemble a panel of hTERT peptides,

rather than a single epitope potentially prone to mutation, suitable for targeting

in immunotherapeutic approaches.

With respect to hTERT, potentially useful TAA peptides will have

scores greater than 150, preferably, greater than 300, more preferably, greater

10   than 500, even more preferably, greater than 1000, still more preferably, greater

than 1500, and most preferably, greater than 1700. In the case of hTERT,

although peptides from any portion of the hTERT amino acid sequence can be

used as a peptide in the methods of the invention, preferred hTERT peptides are

from the amino acid region that spans amino acid 350 through amino acid

15   1000; this amino acid region contains conserved telomerase-specific and RT

motifs, and, hence, tumors that express hTERT are less likely to acquire

mutations in this region, thereby evading an hTERT-specific immune response.

Although 8-mer TAA peptides can be used in the methods of the invention, 9-

mer and 10-mer peptides are preferred.

20   Peptide motif scoring systems can also be used to identify useful 9-mer

and 10-mer TAA peptides that contain substitutions at up to three amino acid

positions. Any substituted peptide that displays a score greater than 150, as is

described above, can be used in the methods of the invention. Table 3 shows

examples of various 9-mer and 10-mer hTERT peptides that can be useful in

25   the methods of the invention, their HLA class I binding partners, and their

relative scores (i.e., estimated half time of dissociation from an HLA molecule

of a molecule containing the hTERT peptide sequence) according to the "HLA

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Peptide Binding Predictions" program.

Other methods for identifying peptides that bind to a histocompatibility antigen of interest are known to those of skill in the art (see, *e.g.*, Paul *Fundamental Immunology* 3rd Edn. Chpt. 17, pages 641-643, 1993, and
5   references cited therein).

To evaluate these candidate peptides as potential CTL epitopes, the following strategy is used. Each peptide is synthesized and tested for binding to the restricted HLA allele. If binding is established, CTL are generated from normal donors, and those cultures able to be expanded are screened for antigen
10   reactivity using peptide-pulsed DC. If antigen-specific CTL are generated, cytotoxicity is tested against a panel of tumor cell lines with diverse histologies. For each peptide, these studies establish whether the peptide (1) binds to the appropriate MHC Class I molecule, (2) is processed by tumor cells such that antigen-derived peptides are available for binding to MHC molecules,
15   and (3) is recognized by the T cell repertoire in an MHC-restricted fashion such that naive CTL precursors bearing specific T cell receptors can be expanded.

Peptides are synthesized by, for example, Fmoc methods (Sigma Genosys). Binding to HLA-A*0201 is measured using the TAP-deficient T2 hybridoma cell line, whose limited HLA-A*0201 expression is markedly
20   upregulated by incubation with peptides that bind to HLA-A*0201. In this assay, TAP-deficient T2 cells (ATCC) are pulsed with 50 μg/ml of β2-microglobulin (Sigma) for 18 hours at 37°C. HLA-A*0201 expression is then measured by flow cytometry using mAb BB7.2 (ATCC), followed by incubation with FITC-conjugated F(ab')$_2$ goat anti-mouse Ig (Zymed).

25   To assess peptide binding to other HLA alleles, T2 transfectant cells expressing other Class I molecules are used along with antibodies specific for these particular alleles.

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Table 2. Candidate hTERT peptides predicted to bind to HLA-A*0201

HLA	hTERT	Sequence	Score*
A*0201	K1081	KLTRHRVTYV (SEQ ID NO:8)	3079
	L933	LLLDTRTLEV (SEQ ID NO:9)	1794
	F544	FLHWLMSVYV (SEQ ID NO:10)	1760
	F1078	FLLKLTRHRV (SEQ ID NO:11)	1184
	W547	WLMSVYVVEL (SEQ ID NO:12)	836
	G804	GLFDVFLRFM (SEQ ID NO:13)	725
	L152	LLARCALFV (SEQ ID NO:14)	650
	W1072	WLCHQAFLL (SEQ ID NO:15)	570
	V554	VELLRSFFYV (SEQ ID NO:16)	516

Positive Control

MAGE-3 271-79	FLWGPRALV (SEQ ID NO:17)	2655
HTLV-1 tax 11-19	LLFGYPVYV (SEQ ID NO:18)	2406
Hbv cAg 18-27	FLWGPRALV (SEQ ID NO:19)	2310
Inf MP 58-66	GILGFVFTL (SEQ ID NO:20)	551

* Calculated score is a predicted estimate of dissociation half-time (minutes) for the peptide binding to HLA. For any particular allele, the threshold for scores predictive of peptide binding is determined by evaluating the scores of viral- or tumor-derived positive control peptides known to bind to the allele (http://www.uni-tuebingen.de/uni/kxi/class1.htm). Additional candidate HLA-2 binding, hTERT peptides are presented in Table 4, below.

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Table 3. Candidate hTERT peptides predicted to bind to non-HLA-A2 alleles

HLA	hTERT peptide	Sequence	Score*
A1	Y325	YAETKHFLY (SEQ ID NO:21)	225
	V553	VVELLRSFFY (SEQ ID NO:22)	225
	I1036	ISDTASLCY (SEQ ID NO:23)	187
	Positive Controls		
	MAGE-3 168-76	EVDPIGHLY (SEQ ID NO:24)	250
	Inf. A NP 44-52	CTELKLSDY (SEQ ID NO:25)	112
A3	G804	GLFDVFLRF (SEQ ID NO:26)	270
	K973	KLFGVLRLK (SEQ ID NO:2)	101
	R535	RLREEILAK (SEQ ID NO:27)	90
	Positive Controls		
	Inf. A. NP 265-73	ILRGSVAHK (SEQ ID NO:28)	90
A11	Y562	YVTETTFQK (SEQ ID NO:29)	6.0
	Q995	QTVCTNIYK (SEQ ID NO:30)	3.0
	K881	KTFLRTLVR (SEQ ID NO:31)	2.4
	R535	RLREEILAK (SEQ ID NO:32)	2.4
	Positive Controls		
	HIV-1 p24 349-59	GVGGPGGHK (SEQ ID NO:33)	6.0
	EBNA-4 416-24	IVTDFSVIK (SEQ ID NO:34)	2.0
A24	T1088	TYVPLLGSL (SEQ ID NO:35)	432
	C845	CYGDMENKL (SEQ ID NO:36)	316

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F575	FYRKSVWSKL (SEQ ID NO:37)	308
A165	AYQVCGPPL (SEQ ID NO:38)	300

<u>Positive Controls</u>

HIV-1 gp41 583-91	RYLKDQQLL (SEQ ID NO:39)	720
P15/mel Ag 10-18	AYGLDFYIL (SEQ ID NO:40)	240

*Calculated score is a predicted estimate of dissociation half-time (minutes) for the peptide binding to HLA. For any particular allele, the threshold for scores predictive of peptide binding is determined by evaluating the scores of viral- or tumor-derived positive control peptides known to bind to the allele (http://www.uni-tuebingen.de/uni/kxi/class1.htm).

Table 4

Additional Candidate HLA-2 binding, hTERT peptides

R572	RLFFYRKSV (SEQ ID NO:41)	L675	LLGASVLGL (SEQ ID NO:52)	K511	KMSVRGCAWL (SEQ ID NO:63)
L1017	LQLPGHQQV (SEQ ID NO:42)	C76	CLKELVARV (SEQ ID NO:53)	R87	RLCERGAKNV (SEQ ID NO:64)
R30	RLGPQGWRL (SEQ ID NO:43)	L934	LLDTRTLEV (SEQ ID NO:54)	L139	LLLRRVGDDV (SEQ ID NO:65)
S504	SLQELTWKM (SEQ ID NO:44)	G932	GLLLDTRTL (SEQ ID NO:55)	G674	GLLGASVLGL (SEQ ID NO:66)
N95	NVLAFGFAL (SEQ ID NO:45)	F88	FLRTLVRGV (SEQ ID NO:56)	L1005	LLLQAYRFHA (SEQ ID NO:67)
V407	VLLKTHCPL (SEQ ID NO:46)	Y772	YMRQFVAHL (SEQ ID NO:57)	K1106	KLPGTTLTAL (SEQ ID NO:68)
F870	FLLVTPHLT (SEQ ID NO:47)	R724	RLTEVIASI (SEQ ID NO:58)	V1070	VQWLCHQAFL (SEQ ID NO:69)
T765	TLTDLQPYM (SEQ ID NO:48)	Q1024	QVWKNPTFFL (SEQ ID NO:59)	A49	ALVAQCLVCV (SEQ ID NO:70)

I836	ILSTLLCSL	V1016	VLQLPFHQQV	R865	RLVDDFLLVT
	(SEQ ID NO:49)		(SEQ ID NO:60)		(SEQ ID NO:71)
L548	LMSVYVVEL	F345	FLLSSLRPSL	S835	SILSTLLCSL
	(SEQ ID NO:50)		(SEQ ID NO:61)		(SEQ ID NO:72)
F986	FLDLQVNSL	L862	LLLRLVDDFL		
	(SEQ ID NO:51)		(SEQ ID NO:62)		

This assay can also be applied to other non-HLA-A2 alleles. T2 cells are transfected with genes from additional class I alleles and selected for stable expression using techniques as described (Anderson *et al.*, J. Immunol. 151:3407-3419, 1993). Importantly, the generation of only a few types of T2 HLA transfectants (*e.g.*, a panel including A*0101, A*0301, A*1101, and A*2401 transfectants in addition to wild-type T2 cells) allows determination of epitopes relevant to more than 95% of cancer patients.

CTL are generated from normal donors according to a protocol of DC/CD40-B cell activation we have previously described (Schultze *et al.*, J. Clin. Invest. 100:2757-2765, 1997; see above). In this system, DC are prepared from peripheral blood using IL4 and GM-CSF. B cells are activated and cultured *via* CD40, as described (Schultze *et al.*, J. Clin. Invest. 100:2757-2765, 1997). After 7 days in culture, DC are harvested, pulsed with peptide (40 μg/ml) and β2-microglobulin (3 μg/ml) for 4 hours at 37°C, irradiated (33 Gy), and added to autologous CD8-enriched T cells at a T:DC ratio of 20:1 in RPMI media with 10% human AB serum, 2 mM glutamine, 15 μg/ml gentamicin, 20 mM HEPES, and 10 ng/ml IL7 (Endogen). At day 7 and weekly thereafter, T cell cultures are harvested and restimulated with irradiated (33Gy), peptide-pulsed autologous CD40-activated B cells, as described (Schultze *et al.*, J. Clin. Invest. 100:2757-2765, 1997). IL2 (50 U/ml; Collaborative Biomedical

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Products) is introduced on day 8 and replenished as needed every 3-4 days.
Cultures are evaluated for cell surface expression of CD3, CD4, CD8, CD56,
CD19, and CD20 after the third or fourth restimulation and subsequently
analyzed for cytotoxicity in standard chromium release assays.

5   For the initial screen of CTL specificity, autologous peptide-pulsed DC
are used as screening targets. DC are telomerase-negative, whereas other
screening targets (e.g., activated B cells or T2 cells) are telomerase-positive and
cannot be used in peptide pulsing experiments (see below). DC pulsed with
control peptides are used as a negative screening target. Four-hour Cr^{51} -

10   release assays are performed in triplicate per condition using 5 x 10^3 labeled
target cells per well in a 96-well plate. Percent specific lysis is calculated from
cpm of (experimental result - spontaneous release)/(maximum release -
spontaneous release).

         In addition, for hTERT peptides predicted to bind to HLA-A*0201, CTL

15   cytotoxicity is reevaluated using as screening targets the osteosarcoma cell line
U20S, previously infected with hTERT or retroviral vector alone (see below).
Wild-type U20S is a rare tumor cell line that is telomerase-negative (Bryan et
al., Nat. Med. 3:1271, 1997). HTERT-specific lysis is reflected by lysis of the
hTERT-infected U20S cells in the absence of lysis of vector-only infected

20   U20S cells. Finally, as CTL specific for hTERT peptides are generated, they
are tested for cytotoxicity against a panel of wild-type tumor cell lines from a
wide range of histologies. Such a panel was used to characterize the I540
hTERT peptide, and includes combinations of carcinoma, melanoma, myeloma,
and EBV-transformed B cell lines that control for MHC-restriction and

25   hTERT-specificity. These experiments are important not only to evaluate
whether the additional hTERT epitopes identified are naturally processed and
presented by tumor cells, but also to test the "universality" of each epitope in a

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range of histologies.

Finally, CTL elaboration of cytokines is also measured following CTL exposure to hTERT peptides and MHC. This exposure can be achieved using peptide-pulsed DC, or, in the case of HLA-A*0201, the infected and control

5   U2OS cells. Assays to measure INFγ and TNF follow previously described methods (Schultze et al., J. Clin. Invest. 100:2757-2765, 1997). It is important to compare hTERT-specific CTL cytotoxicity with cytokine release, as some studies have suggested that cytokine elaboration of specific CTL has a greater correlation with clinical effect than cytotoxicity responses (see, e.g., Aruga et

10   al., Cancer Immunol. Immunother. 41:317-324, 1995).

In choosing which hTERT peptides to test initially, the first criterion is the efficiency of binding to MHC, as reflected by the relative fluorescence shift in the T2 assay. Secondary criteria include where in the hTERT sequence the peptide is located. Higher priority is placed on peptides found within or near

15   either the "telomerase-specific" motif (residues 556 to 565) or one of the six reverse-transcriptase motifs (starting at residues 621, 631, 704, 823, 862, and 895) (Meyerson et al., Cell 90:643-651, 1997; Nakumura et al., Science 277:955-959, 1997). The reason for this priority is the hypothesis that mutations within these regions, although potentially resulting in resistance to

20   CTL lysis, might disrupt the functional activity of telomerase. Interruption of telomerase activity in wild-type telomerase-positive tumors can be a lethal development (Feng et al., Science 269:1236-1241, 1995).

Higher priority for testing is also assigned to peptides found within regions that contain clusters of other predicted peptides. For example, initial

25   review of hTERT indicates that numerous candidate epitopes for multiple alleles localize to a 50mer stretch of hTERT starting at residue 535. Notably, the I540 peptide previously identified is found within this 50mer. In addition,

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several candidate epitopes are also identified in a 25mer stretch of hTERT

starting at residue 1072, including three potential HLA-A*0201-binding

peptides relatively short regions of hTERT found to contain multiple CTL

epitopes for multiple alleles can be evaluated for immunogenicity both *in vitro*

5   and *in vivo*. Furthermore, such peptides can be analyzed for the simultaneous

inclusion of hTERT-specific T helper cell epitopes restricted to MHC Class II,

as has been done for other CTL antigens such as hepatitis B nucleocapsid

(Ferrari *et al.*, J. Clin. Invest. 88:214-222, 19911). A short polypeptide

containing multiple hTERT-specific Class I and Class II epitopes would be

10   inordinately useful in the design of hTERT-specific immunotherapies.

Evaluation of hTERT-specific CTL generation from the peripheral blood of
cancer patients compared with normal donors

         Prevailing hypotheses emphasize the relative inadequacy of the immune

system in cancer patients. Thus, prior to the present invention it was not clear

15   whether vaccination with tumor antigens, for example, can consistently trigger

clinically effective CTL in the tumor-bearing patient. Likewise, the ability to

generate antigen-specific CTL *ex vivo* may be compromised when precursor

cells for CTL expansion are obtained from cancer patients.

         Cancer patients were HLA-typed and underwent leukopheresis to obtain

20   sufficient numbers of peripheral blood mononuclear cells (PBMC). A hTERT

peptide (K973 KLFGVLRLK; SEQ ID NO:2) was used to generate specific

CTL from CD8-purified cells based on the same DC/CD40-activated B cell

system described above.

         The hTERT-derived peptide K973 (KLFGVLRLK; SEQ ID NO:2) was

25   used to generate K973-specific CTL from a healthy donor and a melanoma

patient. Cytotoxicity against peptide pulsed T2 cells transduced with the HLA-

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A3 gene (T2A3) were used to demonstrate K973 killing, as compared to a NP265 (influenza)-specific CTL from the same donors (Fig. 6). The K973-specific CTL from patient blood killed hTERT$^+$ tumors from multiple histologies, in an HLA-A3 restricted fashion, demonstrating that K973 hTERT

5 peptide is naturally processed and presented by tumor cells (Fig. 7). Also, expansion of hTERT (I540)-specific CTL from patients is as efficient as expansion from normal donors (Fig. 8).

CTL clones can also be obtained from patients specific for hTERT and generation of such clones compared to generation of clones from normal

10 donors. The efficiency of expanding precursor CTL cells as clones are compared to that of expanding bulk CTL cultures containing specific cells. Clones are generated similarly to methods previously described (Brodie *et al.*, Nat. Med. 5:34-58, 1999). CD8$^+$ cells are isolated, primed with peptide-pulsed autologous DC, and re-stimulated once with peptide-pulsed CD40-activated B

15 cells. Culture aliquots are replated at limiting dilution (0.5 to 3 cells/well) with IL2 and irradiated allogeneic PBMC in 96-well plates previously incubated with anti-CD3 mAb. After 14 days, growing colonies are expanded using IL2, anti-CD3 mAb, and irradiated allogeneic PBMC, and tested for hTERT specificity. Expansion efficiency of clones is compared to expansion of bulk

20 CTL cultures. Antigen-specificity of clones is evaluated using the cytotoxic and cytokines studies described above. Finally, expansion efficiency and antigen reactivity of patient-derived clones is compared to that of clones from normal donors.

We have also demonstrated I540-specific CTL from normal donors and

25 patients, using tetramer technology (see above; Fig. 9). CTL lines were stained with tetramers specific for the I540 peptide, showing that between 1% and 4% of CD8$^+$ cells are telomerase specific. Tetramers specific for an irrelevant

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HLA-A2 binding peptide, JS34, was used as a negative control. The frequency

of telomerase specific cells in peripheral blood is less than the limit of tetramer

detection for both normal donors and patients.

II. Use of Universal Tumor Associated Antigens in Therapeutic Methods

5   As is discussed above, the invention provides methods for identifying

universal tumor associated antigens (TAAs) that contain peptides that bind to

MHC and are recognized by cytotoxic T lymphocytes in an MHC-restricted

fashion. These antigens, and in particular the MHC-binding peptides within

them, as well as nucleic acid molecules that encode the antigens and peptides,

10   can be used in a variety of methods for preventing or treating conditions

associated with excessive cell proliferation and expression of a universal TAA,

such as cancer.

          Examples of conditions that can be prevented or treated using the

methods of the invention, include, for example, all cancers, e.g., melanoma,

15   lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, lung cancer,

ovarian cancer, uterine cancer, cervical cancer, prostate cancer, liver cancer,

colon cancer, pancreatic cancer, and brain cancer. Pre-cancerous and non-

cancerous conditions characterized by excessive cell proliferation, and

expression of a universal tumor associated antigen, can be treated using the

20   methods of the invention as well. For example, all carcinomas in situ, e.g.,

ductal carcinoma in situ, lobular carcinoma in situ, and cervical carcinoma in

situ, as well as adenoma and benign polyps can be treated using the methods of

the invention.

          Patients that can be treated using the methods of the invention include

25   those whose conditions are at early, intermediate, or advanced stages of

development. Patients can receive treatment according to the invention before,

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during, or after other types of treatment, such as chemotherapy, radiation, or surgery, or can receive the treatment of the invention in the absence of any other type of treatment. The methods of the invention can also be used as general prophylactic measures; to prevent conditions from arising in patients

5   that are at risk, or have early signs, of developing a condition associated with excessive cellular proliferation, such as cancer; or to prevent recurrence of such a condition. Additional persons that can be treated, in particular, using vaccination methods of the invention (see below), are those who are to donate cells, such as cytotoxic T lymphocytes, for use in the treatment of another (see

10   below).

Central to the prophylactic and therapeutic methods of the invention is the pathway of cell-mediated immunity involving cytotoxic T lymphocytes (CTLs). In this pathway, an antigen is taken up and processed by an antigen presenting cell, so that a peptide of the antigen is presented on the surface of

15   the cell, in the context of MHC. Such antigen presenting cells then activate cytotoxic T lymphocytes, in an MHC-restricted fashion, to proliferate and kill target cells that express the antigen.

The prophylactic and therapeutic methods of the invention intervene in this pathway at different levels. For example, in one of these methods, an

20   antigen is administered to a patient, in whom the antigen is taken up by antigen presenting cells, which in turn activate CTLs. In another of these methods, an antigen presenting cell is contacted with an antigen *ex vivo*, where it takes up, processes, and presents the antigen, in the context of MHC. Such *ex vivo* stimulated APCs are then administered to a patient, in whom they specifically

25   activate CTLs. In yet another of these methods, CTLs are activated *ex vivo* with APCs presenting tumor associated antigen peptides, and the activated CTLs are then administered to a patient. These methods, each of which

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includes numerous variations, are described in further detail below.

As is noted above, the prophylactic and therapeutic methods of the invention include one in which a universal TAA, or a fragment thereof that binds to MHC, is administered to a patient, in whom the antigen or fragment is

5   taken up by and processed within an antigen presenting cell, which in turn activates a cytotoxic T cell in the patient. This vaccination method can be carried out using one or more universal TAAs (*e.g.*, hTERT), one or more MHC-binding peptides of a single TAA, one or more MHC-binding peptides of more than one universal TAA, or a combination thereof. Optionally, the

10   antigen can be administered in combination with an adjuvant to enhance the anti-TAA immune response, or the antigen can be packaged into a delivery system (see below).

Any reagent including a universal TAA (*e.g.*, hTERT) or MHC-binding peptide thereof can be used for vaccination. These include, without limitation,

15   full length universal TAA, MHC-binding fragments of universal TAAs, as well as fusion proteins including universal TAAs and MHC-binding fragments thereof. Peptides or polypeptides including TAA peptides and polypeptides can include 8, 9, 10, 11, 12, or more amino acid stretches having sequence identity with a region of a reference TAA, such as hTERT. For example, the

20   peptides can include nine amino acid stretches, in which seven, eight, or all nine of the amino acids in the TAA peptide nine amino acid sequence are identical to a region of nine amino acids in TAA. In addition, in the case of hTERT, a TAA peptide or polypeptide can include up to 1132 amino acids that are identical to an amino acid sequence found in hTERT, for example, 9-20,

25   20-40, 40-80, 80-200, 200-500, 500-1131, or 1131-1132 amino acids that are identical to an amino acid sequence found in hTERT. Polypeptides containing TAA (*e.g.*, hTERT) peptides can contain additional amino acid stretches that do

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not correspond to the amino acid sequence of the TAA.

To vaccinate a patient to elicit a universal TAA (*e.g.*, hTERT)-specific

immune response in the patient, it is necessary to obtain large amounts of the

universal TAA protein or peptide, and this can be accomplished by numerous

5   standard methods, for example, chemical synthesis (*e.g.*, Fmoc methods (Sigma

Genosys); see above) or expression in eukaryotic or prokaryotic cells. (These

methods can also be used to produce universal TAAs or MHC-binding peptides

thereof for use in pulsing antigen presenting cells; see below.)

Recombinant TAA peptides, such as hTERT peptides, can be

10   overexpressed *in vivo* by introducing coding sequences of the peptide into

various types of cells, or *in vitro*, using cell-free expression systems that are

known in the art. The peptide products can then purified for generating TAA-

specific CTLs *ex vivo* and for vaccine production. Purified TAA peptides are

also useful for diagnostic assays that measure the presence of TAA-specific

15   CTLs in a test sample. For example, the presence (or increased levels) of

TAA-specific CTLs in a sample from a subject who has received an anti-TAA

vaccination, relative to the level of TAA-specific CTLs in a reference sample

(such as a pre-vaccination sample from the patient), indicates that the patient

has mounted a TAA-specific immune response.

20   TAA peptides, such as hTERT peptides, can be produced by chemical

synthesis (*e.g.*, by the methods described in *Solid Phase Peptide Synthesis*, 2nd

ed., 1984, The Pierce Chemical Co., Rockford, IL, or by other methods known

to those skilled in the art of peptide synthesis).

A wide variety of expression systems can be used to produce

25   recombinant TAA peptides, polypeptides, fragments, fusion proteins, and

amino acid sequence variants. TAA peptides can be produced in prokaryotic

hosts (*e.g.*, *E. coli*) or in eukaryotic hosts (*e.g.*, *S. cerevisiae*, insect cells, such

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as Sf9 cells, or mammalian cells, such as COS-1, NIH 3T3, or HeLa cells).
These cells are commercially available from, for example, the American Type
Culture Collection, Rockville, Maryland (also see, e.g., Ausubel et al., Current
Protocols in Molecular Biology, John Wiley & Sons, New York, NY, 1998).

5   The method of transformation and the choice of expression vehicle (e.g.,
expression vector) depends on the host system selected. Transformation and
transfection methods are described, e.g., by Ausubel et al., supra, and
expression vehicles can be chosen from the numerous examples that are known
in this field.

10   First, a nucleic acid molecule encoding a TAA peptide, such as an
hTERT peptide, is introduced into a plasmid or other vector, which is then used
to transform living cells. Constructs in which a cDNA containing the entire
TAA coding sequence, a fragment of the TAA coding sequence, amino acid
variations of the TAA coding sequence, or fusion proteins of the

15   aforementioned, inserted in the correct orientation into an expression plasmid,
can be used for protein expression. Prokaryotic and eukaryotic expression
systems allow various immunogenic domains of TAA peptides or polypeptides
to be recovered as fusion proteins, and then used for the generation of TAA-
specific CTLs. In some cases, for example, when a TAA peptide is to be

20   expressed directly within a patient's cells, it may be desirable to express the
TAA peptide under the control of an inducible or tissue-specific promoter.

         Typical expression vectors contain promoters that direct the synthesis of
large amounts of mRNA corresponding to the inserted TAA peptide-encoding
nucleic acid molecule in the plasmid-bearing cells. They can also include

25   eukaryotic or prokaryotic "origin of replication" sequences, which allow for
their autonomous replication within the host organism, sequences that encode
genetic traits that allow vector-containing cells to be selected in the presence of

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otherwise toxic drugs (such as antibiotics), and sequences that increase the efficiency with which the synthesized mRNA is translated. Stable, long-term vectors can be maintained as freely replicating entities within cells by using regulatory elements of, for example, viruses (*e.g.*, the OriP sequences from the

5   Epstein Barr Virus genome). Cell lines can also be produced that have the vector integrated into genomic DNA, and, in this manner, the gene product is produced on a continuous basis.

Expression of foreign sequences in bacteria such as *Escherichia coli* requires insertion of a nucleic acid molecule encoding a polypeptide into a

10   bacterial expression vector. Plasmid vectors in this category contain several elements required for propagation of the plasmid in bacteria and expression of inserted DNA of the plasmid by the plasmid-carrying bacteria. Propagation of only plasmid-bearing bacteria is achieved by introducing into the plasmid selectable marker-encoding sequences that allow plasmid-bearing bacteria to

15   grow in the presence of otherwise toxic drugs (*e.g.*, antibiotics). The plasmid also includes a transcriptional promoter that capable of producing large amounts of mRNA from the cloned gene. Such promoter may or may not be inducible promoters. The plasmid also, preferably, contains a polylinker to simplify insertion of the gene in the correct orientation within the vector. For

20   example, in a simple *E. coli* expression vector utilizing the lac promoter, the expression vector plasmid contains a fragment of the *E. coli* chromosome containing the lac promoter and the neighboring *lacZ* gene. In the presence of the lactose analog IPTG, RNA polymerase normally transcribes the *lacZ* gene, producing *lacZ* mRNA, which is translated into the encoded protein, β-

25   galactosidase. The *lacZ* gene can be cut out of the expression vector with restriction endonucleases and replaced by a TAA (*e.g.*, hTERT) peptide gene sequence, or a fragment, fusion, or mutant thereof. When the resulting plasmid

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is transfected into *E. coli*, addition of IPTG and subsequent transcription from the lac promoter produces mRNA encoding the polypeptide of interest, which is then translated into a polypeptide.

Once the appropriate expression vector containing a TAA (*e.g.*, hTERT)

5   gene is constructed, it is introduced into an appropriate host cell by transformation, transfection, or transduction techniques that are known in the art, including calcium chloride transformation, calcium phosphate transfection, DEAE-dextran transfection, electroporation, microinjection, protoplast fusion, and liposome-mediated transfection. The host cells that are transformed with

10   the vectors of this invention can include (but are not limited to) *E. coli* or other bacteria, yeast, fungi, insect cells (using, for example, baculoviral vectors for expression), human, mouse, or other animal cells. Mammalian cells can also be used to express TAA peptides using a vaccinia virus expression system, as is described by Ausubel *et al.*, *supra*.

15   *In vitro* expression of TAA (*e.g.*, hTERT) peptides, proteins, fusions, polypeptide fragments, or mutated versions thereof encoded by cloned DNA is also possible using the T7 late promoter expression system. Plasmid vectors containing late promoters and the corresponding RNA polymerases from related bacteriophages such as T3, T5, and SP6 can also be used for *in vitro*

20   production of proteins from cloned DNA. *E. coli* can also be used for expression using an M13 phage such as mGPI-2. Furthermore, vectors that contain phage lambda regulatory sequences, or vectors that direct the expression of fusion proteins, for example, a maltose-binding protein fusion protein or a glutathione-S-transferase fusion protein, also can be used for

25   expression in *E. coli*.

Eukaryotic expression systems permit appropriate post-translational modifications to expressed proteins. Transient transfection of a eukaryotic

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expression plasmid allows the transient production of TAA peptides by a

transfected host cell. TAA peptides can also be produced by a stably-

transfected mammalian cell line. A number of vectors suitable for stable

transfection of mammalian cells are available to the public (*e.g.*, see Pouwels *et*

5   *al.*, *Cloning Vectors: A Laboratory Manual*, 1985, Supp. 1987), as are methods

for constructing such cell lines (see, *e.g.*, Ausubel *et al.*, *supra*). In one

example, cDNA encoding a TAA (*e.g.*, hTERT) peptide, protein, fragment,

mutant, or fusion protein is cloned into an expression vector that includes the

dihydrofolate reductase (DHFR) gene. Integration of the plasmid and,

10   therefore, integration of the TAA peptide-encoding gene into the host cell

chromosome is selected by inclusion of 0.01-300 µM methotrexate in the cell

culture medium (as is described by Ausubel *et al.*, *supra*). This dominant

selection can be accomplished in most cell types. Recombinant protein

expression can be increased by DHFR-mediated amplification of the

15   transfected gene. Methods for selecting cell lines bearing gene amplifications

are described by Ausubel *et al.*, *supra*. These methods generally involve

extended culture in medium containing gradually increasing levels of

methotrexate. The most commonly used DHFR-containing expression vectors

are pCVSEII-DHFR and pAdD26SV(A) (described by Ausubel *et al.*, *supra*).

20   The host cells described above or, preferably, a DHFR-deficient CHO cell line

(*e.g.*, CHO DHFR⁻ cells, ATCC Accession No. CRL 9096) are among those

most preferred for DHFR selection of a stably-transfected cell line or DHFR-

mediated gene amplification. Other drug markers can be analogously used.

Expression of proteins, such as those containing TAA (*e.g.*, hTERT)

25   peptides, in eukaryotic cells allows the production of large amounts of normal

or mutant proteins for isolation and purification, and the use of cells expressing

a TAA peptide-containing protein provides a functional assay system for

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antibodies generated against the TAA peptide of interest.

Another preferred eukaryotic expression system is the baculovirus system using, for example, the vector pBacPAK9, which is available from Clontech (Palo Alto, CA). If desired, this system can be used in conjunction with other protein expression techniques, for example, the myc tag approach described by Evan *et al.* (Mol. Cell Biol. 5:3610-3616, 1985).

Once a recombinant protein is expressed, it can be isolated from the expressing cells by cell lysis followed by protein purification techniques, such as affinity chromatography. In this example, an anti-TAA peptide antibody, which can be produced by methods that are well-known in the art, can be attached to a column and used to isolate recombinant TAA peptide-containing proteins. Lysis and fractionation of TAA peptide-harboring cells prior to affinity chromatography can be performed by standard methods (see, *e.g.*, Ausubel *et al., supra*). Once isolated, the recombinant protein can, if desired, be purified further, *e.g.*, by high performance liquid chromatography (HPLC; *e.g.*, see Fisher, *Laboratory Techniques in Biochemistry and Molecular Biology*, Work and Burdon, Eds., Elsevier, 1980).

Preferably, the universal TAA antigen or MHC-binding peptide thereof is administered to a patient in association with an adjuvant. For example, a chemical antigen (*e.g.*, Freund's incomplete adjuvant; cytoxan; an aluminum compound, such as aluminum hydroxide, aluminum phosphate, or aluminum hydroxyphosphate; liposomes; ISCOMS; microspheres; protein chochleates; vesicles consisting of nonionic surfactants; cationic amphiphilic dispersions in water; oil/water emulsions; muramidyldipeptide (MDP) and its derivatives such as glucosyl muramidyldipeptide (GMDP), threonyl-MDP, murametide and murapalmitin; and QuilA and its subfractions; as well as various other compounds such as monophosphoryl-lipid A (MPLA); gamma-inulin;